

GenCore version 5.1.7
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OM nucleic - nucleic search, using BW model

Run on: April 1, 2006, 06:12:08 ; Search time 17.7662 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-9

Perfect score: 20
Sequence: 1 tagtaccctaataacta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 segs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match of
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New:*
1: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
10: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------|
| 1 | 17.4 | 87.0 | 511 | 9 | US-10-301-480-56566 |
| 2 | 17.4 | 87.0 | 511 | 9 | US-10-301-480-669975 |
| 3 | 17.4 | 87.0 | 635 | 6 | US-09-925-065A-563041 |
| 4 | 17.4 | 87.0 | 1323 | 6 | US-09-925-065A-82927 |
| 5 | 17.4 | 87.0 | 1323 | 9 | US-10-301-480-29168 |
| 6 | 17.4 | 87.0 | 1323 | 9 | US-10-301-480-184167 |
| 7 | 17.4 | 87.0 | 1323 | 10 | US-10-301-480-642577 |
| 8 | 17.4 | 87.0 | 1323 | 10 | US-10-301-480-642577 |
| 9 | 17.4 | 87.0 | 100137 | 9 | US-10-301-480-797576 |
| C 10 | 17.4 | 87.0 | 139573 | 10 | US-10-506-513-3 |
| C 11 | 16.8 | 84.0 | 629 | 6 | US-09-925-065A-340911 |
| C 12 | 16.8 | 84.0 | 629 | 6 | US-09-925-065A-340912 |
| C 13 | 16.8 | 84.0 | 629 | 6 | US-09-925-065A-340913 |
| C 14 | 16.8 | 84.0 | 642 | 6 | US-09-925-065A-340914 |
| C 15 | 16.8 | 84.0 | 646 | 10 | US-10-301-480-413849 |
| C 16 | 16.8 | 84.0 | 646 | 10 | US-10-301-480-413850 |
| C 17 | 16.8 | 84.0 | 646 | 10 | US-10-301-480-413851 |
| C 18 | 16.8 | 84.0 | 646 | 10 | US-10-301-480-1027258 |

| | | | | | | |
|------|------|------|------|----|-----------------------|--------------------|
| C 19 | 16.8 | 84.0 | 646 | 10 | US-10-301-480-1027259 | Sequence 1027259, |
| C 20 | 16.8 | 84.0 | 646 | 10 | US-10-301-480-1027260 | Sequence 1027260, |
| C 21 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717969 | Sequence 717969, |
| C 22 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717970 | Sequence 717970, |
| C 23 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717971 | Sequence 717971, |
| C 24 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717972 | Sequence 717972, |
| C 25 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717973 | Sequence 717973, |
| C 26 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717974 | Sequence 717974, |
| C 27 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717975 | Sequence 717975, |
| C 28 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717976 | Sequence 717976, |
| C 29 | 16.8 | 84.0 | 3094 | 6 | US-09-925-065A-717977 | Sequence 717977, |
| C 30 | 16.4 | 82.0 | 700 | 6 | US-09-925-065A-688196 | Sequence 688196, |
| C 31 | 16 | 80.0 | 970 | 8 | US-10-750-185-30148 | Sequence 30148, A |
| C 32 | 16 | 80.0 | 970 | 8 | US-10-750-623-30148 | Sequence 30148, A |
| C 33 | 15.8 | 79.0 | 462 | 6 | US-09-925-065A-420236 | Sequence 420236, |
| C 34 | 15.8 | 79.0 | 473 | 10 | US-10-301-480-485240 | Sequence 485240, |
| C 35 | 15.8 | 79.0 | 473 | 10 | US-10-301-480-1096649 | Sequence 1096649, |
| C 36 | 15.8 | 79.0 | 473 | 10 | US-10-301-480-129900 | Sequence 129900, A |
| C 37 | 15.8 | 79.0 | 511 | 9 | US-10-301-480-527309 | Sequence 627309, |
| C 38 | 15.8 | 79.0 | 511 | 10 | US-10-301-480-243647 | Sequence 243647, |
| C 39 | 15.8 | 79.0 | 513 | 10 | US-10-301-480-243648 | Sequence 243648, |
| C 40 | 15.8 | 79.0 | 513 | 10 | US-10-301-480-857056 | Sequence 857056, |
| C 41 | 15.8 | 79.0 | 513 | 10 | US-10-301-480-857057 | Sequence 857057, |
| C 42 | 15.8 | 79.0 | 517 | 6 | US-09-925-065A-149561 | Sequence 149561, |
| C 43 | 15.8 | 79.0 | 517 | 6 | US-09-925-065A-149562 | Sequence 149562, |
| C 44 | 15.8 | 79.0 | 517 | 14 | US-11-136-527-3431 | Sequence 3431, Ap |
| C 45 | 15.8 | 79.0 | 517 | 14 | US-11-136-527-7527 | Sequence 7527, Ap |

ALIGNMENTS

RESULT 1
US-10-301-480-56566
Sequence 56566, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56566
LENGTH: 511
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-56566

Query Match 87.0% ; Score 17.4 ; DB 9 ; Length 511 ;
Best Local Similarity 94.7% ; Pred. No. 29 ;
Matches 18 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

Qy 1 TAGTACCCTAATTAACCT 19
Db 432 TAGTTCCTAATTAACCT 450

RESULT 2
US-10-301-480-669975
Sequence 669975, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 3.99328 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-9

Perfect score: 20

Sequence: 1 tagtaccctaattaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patente NA: *
2: /cgn2_6/ptodaca/1/ina/1 COMB.seq: *
3: /cgn2_6/ptodaca/1/ina/5 COMB.seq: *
4: /cgn2_6/ptodaca/1/ina/6A COMB.seq: *
5: /cgn2_6/ptodaca/1/ina/6B COMB.seq: *
6: /cgn2_6/ptodaca/1/ina/6C COMB.seq: *
7: /cgn2_6/ptodaca/1/ina/PP COMB.seq: *
8: /cgn2_6/ptodaca/1/ina/RB COMB.seq: *
9: /cgn2_6/ptodaca/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|----------------------|--------------------|
| 1 | 16.4 | 82.0 67386 3 | US-09-949-016-16519 | Sequence 16519, A |
| 2 | 15.8 | 79.0 601 3 | US-09-949-016-133604 | Sequence 133604, A |
| 3 | 15.8 | 79.0 212139 3 | US-09-949-016-16065 | Sequence 16065, A |
| 4 | 15.8 | 79.0 245286 3 | US-09-949-016-15497 | Sequence 15497, A |
| 5 | 15.2 | 76.0 601 3 | US-09-949-016-171671 | Sequence 171671, A |
| 6 | 15.2 | 76.0 601 3 | US-09-949-002-4497 | Sequence 4497, Ap |
| 7 | 15.2 | 76.0 1540 3 | US-09-071-035-67 | Sequence 67, Appl |
| 8 | 15.2 | 76.0 1540 3 | US-10-206-576-67 | Sequence 65, Appl |
| 9 | 15.2 | 76.0 1707 3 | US-09-071-035-65 | Sequence 65, Appl |
| 10 | 15.2 | 76.0 1803 3 | US-09-134-000C-2881 | Sequence 2881, Ap |
| 11 | 15.2 | 76.0 3722 3 | US-10-164-595-9 | Sequence 9, Appl |
| 12 | 15.2 | 76.0 3862 3 | US-10-164-595-5 | Sequence 5, Appl |
| 13 | 15.2 | 76.0 3937 3 | US-10-164-595-7 | Sequence 7, Appl |
| 14 | 15.2 | 76.0 3985 3 | US-10-164-595-3 | Sequence 3, Appl |
| 15 | 15.2 | 76.0 36755 3 | US-09-949-016-16994 | Sequence 16994, A |
| 16 | 15.2 | 76.0 36059 3 | US-09-328-925-4 | Sequence 4, Appl |
| 17 | 15.2 | 76.0 91062 3 | US-09-949-016-13019 | Sequence 13019, A |
| 18 | 15.2 | 76.0 185765 3 | US-09-949-002-674 | Sequence 674, App |
| 19 | 15.2 | 76.0 185765 3 | US-09-949-002-707 | Sequence 707, App |
| 20 | 15.2 | 76.0 298336 3 | US-09-949-016-16600 | Sequence 16600, A |
| 21 | 15.2 | 76.0 421491 3 | US-09-949-016-12805 | Sequence 12805, A |
| 22 | 15.2 | 76.0 421491 3 | US-09-949-016-14060 | Sequence 14060, A |
| 23 | 15.2 | 76.0 455726 3 | US-09-949-016-14157 | Sequence 14157, A |

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|----|------|----------------|----------------------|--------------------|
| 25 | 15.2 | 76.0 481115 3 | US-09-949-016-11940 | Sequence 11940, A |
| 26 | 15.2 | 76.0 1230025 3 | US-09-198-452A-1 | Sequence 1, Appl |
| 27 | 15.2 | 76.0 1230230 3 | US-09-438-185A-1 | Sequence 1, Appl |
| 28 | 15 | 75.0 601 3 | US-09-949-016-80142 | Sequence 80142, A |
| 29 | 15 | 75.0 312470 3 | US-09-949-016-14043 | Sequence 14043, A |
| 30 | 15 | 75.0 336024 3 | US-09-949-016-12373 | Sequence 12373, A |
| 31 | 14.8 | 74.0 228 3 | US-09-489-039A-5795 | Sequence 5795, Ap |
| 32 | 14.8 | 74.0 252 3 | US-09-489-039A-6239 | Sequence 6239, Ap |
| 33 | 14.8 | 74.0 353 3 | US-09-513-999C-1045 | Sequence 1045, Ap |
| 34 | 14.8 | 74.0 468 3 | US-09-513-999C-10440 | Sequence 10440, A |
| 35 | 14.8 | 74.0 601 3 | US-09-949-016-26221 | Sequence 26221, A |
| 36 | 14.8 | 74.0 601 3 | US-09-949-016-35377 | Sequence 35377, A |
| 37 | 14.8 | 74.0 601 3 | US-09-949-016-41896 | Sequence 41896, A |
| 38 | 14.8 | 74.0 601 3 | US-09-949-016-56207 | Sequence 56207, A |
| 39 | 14.8 | 74.0 601 3 | US-09-949-016-74123 | Sequence 74123, A |
| 40 | 14.8 | 74.0 601 3 | US-09-949-016-74154 | Sequence 74154, A |
| 41 | 14.8 | 74.0 601 3 | US-09-949-016-123831 | Sequence 123831, A |
| 42 | 14.8 | 74.0 601 3 | US-09-949-016-205672 | Sequence 205672, A |
| 43 | 14.8 | 74.0 807 3 | US-09-270-767-29121 | Sequence 29121, A |
| 44 | 14.8 | 74.0 815 3 | US-09-328-111-23 | Sequence 23, Appl |
| 45 | 14.8 | 74.0 1322 3 | US-09-270-767-4286 | Sequence 4286, Ap |

ALIGNMENTS

RESULT 1
US-09-949-016-16519
Sequence 16519, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ. ID NOS: 207012
SOFTWARE: PaacSeq for Windows Version 4.0
SEQ ID NO 16519
LENGTH: 67386
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(67386)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16519

Query Match 82.0%; Score 16.4; DB 3; Length 67386;
Best local similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0;

Qy 3 GTTACCTATTACCTA 20
Db 48082 GTTACCTATTACCTA 48099

RESULT 2
US-09-949-016-133604/C
Sequence 133604, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307

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OM nucleic - nucleic search, using bw model

Run on: April 1, 2006, 05:54:26 ; Search time 114.438 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagtaccctaataccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_ests1:
2: gb_ests2:
3: gb_ests3:
4: gb_hcc:
5: gb_ests4:
6: gb_ests5:
7: gb_ests6:
8: gb_ests7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 20 | 100.0 | 188 | 10 | BX206435 Danio rer |
| 2 | 20 | 100.0 | 297 | 3 | BM153964 f37b09.x |
| 3 | 20 | 100.0 | 297 | 10 | BX206839 Danio rer |
| 4 | 20 | 100.0 | 323 | 10 | BX212086 Danio rer |
| 5 | 20 | 100.0 | 390 | 11 | DR33K5T |
| 6 | 20 | 100.0 | 509 | 7 | CK698900 zrf101-P00 |
| 7 | 20 | 100.0 | 510 | 3 | BI879062 fml8e06.x |
| 8 | 20 | 100.0 | 512 | 11 | DR41D2S |
| 9 | 20 | 100.0 | 548 | 10 | BX130901 Danio rer |
| 10 | 20 | 100.0 | 556 | 10 | BX154360 Danio rer |
| 11 | 20 | 100.0 | 564 | 11 | DR114S |
| 12 | 20 | 100.0 | 589 | 11 | DR34F2S |
| 13 | 20 | 100.0 | 693 | 10 | BX191816 Danio rer |
| 14 | 20 | 100.0 | 707 | 8 | DN899849 nap49h10. |
| 15 | 20 | 100.0 | 727 | 10 | BX192126 Danio rer |
| 16 | 20 | 100.0 | 728 | 10 | BX221887 Danio rer |
| 17 | 20 | 100.0 | 770 | 7 | CF998030 AGENCOURT |
| 18 | 20 | 100.0 | 771 | 10 | BX205393 Danio rer |
| 19 | 20 | 100.0 | 772 | 10 | BX177611 Danio rer |
| 20 | 20 | 100.0 | 776 | 7 | CNS11985 AGENCOURT |
| 21 | 20 | 100.0 | 781 | 10 | BX220046 Danio rer |
| 22 | 20 | 100.0 | 785 | 10 | BX137180 Danio rer |

| | | | | | | |
|---|----|----|-------|-----|----|--------------------|
| c | 23 | 20 | 100.0 | 797 | 10 | BX234965 Danio rer |
| c | 24 | 20 | 100.0 | 802 | 7 | BX129731 Danio rer |
| c | 25 | 20 | 100.0 | 805 | 7 | CNS05208 AGENCOURT |
| c | 26 | 20 | 100.0 | 812 | 10 | BX223505 Danio rer |
| c | 27 | 20 | 100.0 | 821 | 10 | BX206804 Danio rer |
| c | 28 | 20 | 100.0 | 824 | 10 | BX156069 Danio rer |
| c | 29 | 20 | 100.0 | 831 | 7 | CN170393 AGENCOURT |
| c | 30 | 20 | 100.0 | 861 | 6 | CD760369 AGENCOURT |
| c | 31 | 20 | 100.0 | 896 | 6 | CF594812 AGENCOURT |
| c | 32 | 20 | 100.0 | 919 | 6 | CA474743 AGENCOURT |
| c | 33 | 20 | 100.0 | 934 | 6 | CA474833 AGENCOURT |
| c | 34 | 20 | 100.0 | 950 | 10 | BX158466 Danio rer |
| c | 35 | 20 | 100.0 | 950 | 10 | BX247732 Danio rer |
| c | 36 | 20 | 100.0 | 950 | 10 | BM024443 f47d09.y |
| c | 37 | 20 | 100.0 | 950 | 11 | DR48H1OT |
| c | 38 | 20 | 100.0 | 708 | 8 | DN857131 AGENCOURT |
| c | 39 | 20 | 100.0 | 758 | 6 | CB571304 AGENCOURT |
| c | 40 | 20 | 100.0 | 813 | 10 | BX210720 Danio rer |
| c | 41 | 20 | 100.0 | 857 | 10 | BX181115 Danio rer |
| c | 42 | 20 | 100.0 | 228 | 3 | BI845756 f896h05.x |
| c | 43 | 20 | 100.0 | 244 | 10 | BX131174 Danio rer |
| c | 44 | 20 | 100.0 | 269 | 10 | BX232465 Danio rer |
| c | 45 | 20 | 100.0 | 271 | 10 | BX244148 Danio rer |

ALIGNMENTS

RESULT 1
LOCUS BX206435 188 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEX-238J19, genomic survey sequence.
ACCESSION BX206435
VERSION BX206435.1 GI:28038321
KEYWORDS GSS.

SOURCE
ORGANISM Danio rerio (zebrafish)

REFERENCE
AUTHORS Humphray, S.J., Huckle, B. and Durham, J.L.
TITLE 1 (bases 1 to 188)
JOURNAL Cypriniformes; Cyprinidae; Danio.

COMMENT
Submitted (27-JUN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 238J19. 238J19 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details:

http://www.sanger.ac.uk/Projects/D_rerio/..

FEATURES
source Location/Qualifiers

1..188
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-238J19"
/cruise_type="Testis"
/note="vector pindigBAC-536"

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 188;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGTACCTAATTAACCTA 20
Db 55 TAGTACCTAATTAACCTA 74

RESULT 2
LOCUS BM153964 297 bp mRNA linear EST 30-NOV-2001
DEFINITION f37b09.x1 Sugano SOD adult male Danio rerio cDNA clone

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 16.3691 Seconds
(Without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-9

Sequence: 1 tagttacccttaactaacta 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseg_21:*
2: Geneseg_1980s:*
3: Geneseg_1990s:*
4: Geneseg_2000s:*
5: Geneseg_2001as:*
6: Geneseg_2002as:*
7: Geneseg_2002bs:*
8: Geneseg_2003as:*
9: Geneseg_2003bs:*
10: Geneseg_2003cs:*
11: Geneseg_2003ds:*
12: Geneseg_2004as:*
13: Geneseg_2004bs:*
14: Geneseg_2005as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|--------|--------------------|
| 1 | 20 | 100.0 | 20 | ADT08250 Zebrafish |
| 2 | 20 | 100.0 | 20 | ADT89058 Zebrafish |
| 3 | 20 | 100.0 | 435 | ADT08242 Zebrafish |
| 4 | 20 | 100.0 | 435 | ADT89050 Zebrafish |
| 5 | 20 | 100.0 | 480 | ADT08271 Zebrafish |
| 6 | 20 | 100.0 | 480 | ADT89079 Zebrafish |
| 7 | 20 | 100.0 | 2033 | ADT08244 Zebrafish |
| 8 | 20 | 100.0 | 2033 | ADT89052 Zebrafish |
| 9 | 20 | 100.0 | 2783 | ADT08243 Zebrafish |
| 10 | 20 | 100.0 | 2783 | ADT89051 Zebrafish |
| 11 | 20 | 100.0 | 2960 | ADT89080 Zebrafish |
| 12 | 18.4 | 92.0 | 3003 | ADT18692 Zebrafish |
| 13 | 18.4 | 92.0 | 13382 | ADW44488 Zebrafish |
| 14 | 18.4 | 92.0 | 13382 | ADW44488 Zebrafish |
| 15 | 17.4 | 87.0 | 100137 | ADQ97643 Human can |
| 16 | 17.4 | 87.0 | 139573 | ADH58564 Human Na+ |
| 17 | 17.4 | 87.0 | 156416 | ABD32817 Human can |
| 18 | 16.8 | 84.0 | 5563 | AAK08941 GATA-1 pr |
| 19 | 16.8 | 84.0 | 8346 | ABR28328 DNA trans |

| | | | | | | |
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| 20 | 16.8 | 84.0 | 78064 | 13 | AD517402 | Ad517402 Nucleotide |
| 21 | 16.8 | 84.0 | 96599 | 10 | AD085298 | Ad085298 Human Egr |
| 22 | 16.8 | 84.0 | 96600 | 10 | ADA02819 | Ada02819 Mouse Sox |
| 23 | 16.8 | 84.0 | 96600 | 10 | ADB72557 | AdB72557 Mouse Sox |
| 24 | 16.8 | 84.0 | 96600 | 12 | ADM74414 | Adm74414 Murine ca |
| 25 | 16.4 | 82.0 | 110000 | 12 | ADN46845_04 | Continuation (5 of |
| 26 | 16.4 | 82.0 | 110000 | 12 | ADN47591_16 | Continuation (17 o |
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| 30 | 16.4 | 82.0 | 110000 | 12 | ADN47960_16 | Continuation (17 o |
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| 32 | 15.8 | 79.0 | 389 | 10 | ACD93134 | ACD93134 Human col |
| 33 | 15.8 | 79.0 | 401 | 4 | AAK95767 | AAK95767 Human neu |
| 34 | 15.8 | 79.0 | 401 | 4 | AAK95766 | AAK95766 Human neu |
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| 39 | 15.8 | 79.0 | 401 | 6 | ABT00537 | Abt00536 Human neu |
| 40 | 15.8 | 79.0 | 401 | 6 | ABT00536 | Abt02030 Human neu |
| 41 | 15.8 | 79.0 | 401 | 6 | ABT02030 | Abt02029 Human neu |
| 42 | 15.8 | 79.0 | 401 | 6 | ABT02029 | Abt02031 Human neu |
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| 45 | 15.8 | 79.0 | 426 | 6 | ABN66455 | |

ALIGNMENTS

RESULT 1
ADT08250 standard; DNA; 20 BP.
ID ADT08250;
AC ADT08250;
DT 13-JAN-2005 (first entry)
XX Zebrafish L-FABP upstream region PDX2 binding site.
XX Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX Danio rerio.
XX US2004209833-A1.
XX 21-OCT-2004.
XX 21-NOV-2003; 2003US-00717573.
XX 16-APR-2003; 2003US-0463035P.
XX 27-MAY-2003; 2003US-0473210P.
XX (WUJ/) WU J.
XX (HERG/) HER G M.
XX Wu J, Her GM;
XX WPI; 2004-765481/75.
XX New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX Claim 5; SEQ ID NO 9; 40pp; English.
XX The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 118.984 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-9

Perfect score: 20
Sequence: 1 tagttaccctaatctaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_in:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 20 | 100.0 | 13481 | 5 | DRE251640 |
| 3 | 20 | 100.0 | 16353 | 5 | CR522254 |
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| 5 | 20 | 100.0 | 39600 | 14 | CR361567 |
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| 7 | 20 | 100.0 | 46016 | 5 | CR381556 |
| 8 | 20 | 100.0 | 51065 | 5 | CR936321 |
| 9 | 20 | 100.0 | 52968 | 5 | BX927067 |
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| 11 | 20 | 100.0 | 55372 | 14 | CR759965 |
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| 13 | 20 | 100.0 | 58279 | 5 | CR854925 |
| 14 | 20 | 100.0 | 58949 | 14 | BX649482_3 |
| 15 | 20 | 100.0 | 61341 | 5 | BX666063 |
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| 18 | 20 | 100.0 | 73207 | 5 | BX914202 |

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| C | 19 | 20 | 100.0 | 73894 | 5 | BX296559 | BX296559 zebrafish |
| | 20 | 20 | 100.0 | 74464 | 5 | BX294187 | BX294187 zebrafish |
| | 21 | 20 | 100.0 | 76812 | 5 | BX855614 | BX855614 zebrafish |
| | 22 | 20 | 100.0 | 80226 | 5 | BX323582 | BX323582 zebrafish |
| | 23 | 20 | 100.0 | 82797 | 14 | BX890561_3 | Continuation (4 of |
| | 24 | 20 | 100.0 | 86183 | 5 | BX469918 | BX469918 zebrafish |
| | 25 | 20 | 100.0 | 87559 | 5 | BX571814 | BX571814 zebrafish |
| | 26 | 20 | 100.0 | 88824 | 5 | CR933839 | CR933839 zebrafish |
| | 27 | 20 | 100.0 | 89050 | 5 | CR536610 | CR536610 zebrafish |
| | 28 | 20 | 100.0 | 90347 | 5 | AL714030 | AL714030 zebrafish |
| | 29 | 20 | 100.0 | 91311 | 5 | CR356238 | CR356238 zebrafish |
| | 30 | 20 | 100.0 | 91343 | 14 | CT009673 | CT009673 Danio rer |
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| | 32 | 20 | 100.0 | 91362 | 5 | BX950869 | BX950869 zebrafish |
| | 33 | 20 | 100.0 | 92348 | 5 | AL935295 | AL935295 zebrafish |
| | 34 | 20 | 100.0 | 92637 | 5 | BX855615 | BX855615 zebrafish |
| | 35 | 20 | 100.0 | 93244 | 14 | CT009621 | CT009621 Danio rer |
| | 36 | 20 | 100.0 | 93602 | 14 | CT009592 | CT009592 Danio rer |
| | 37 | 20 | 100.0 | 94103 | 5 | AL845545 | AL845545 zebrafish |
| | 38 | 20 | 100.0 | 95153 | 5 | CR954248 | CR954248 Danio rer |
| | 39 | 20 | 100.0 | 95674 | 5 | CR759816 | CR759816 zebrafish |
| | 40 | 20 | 100.0 | 95798 | 5 | AL954721 | AL954721 zebrafish |
| | 41 | 20 | 100.0 | 98080 | 14 | CR925801 | CR925801 Danio rer |
| | 42 | 20 | 100.0 | 98080 | 14 | CR925801 | CR925801 Danio rer |
| | 43 | 20 | 100.0 | 98407 | 14 | CR383670 | CR383670 Danio rer |
| | 44 | 20 | 100.0 | 99186 | 14 | AL732580 | AL732580 Danio rer |
| | 45 | 20 | 100.0 | 99186 | 14 | AL732580 | AL732580 Danio rer |

ALIGNMENTS

| | | | | | |
|-------------|--|-------------|-----|--------|-----------------|
| RESULT 1 | AF512998 | 2960 bp | DNA | linear | VRT 10-JUL-2003 |
| LOCUS | Danio rerio liver-type fatty acid binding protein gene, partial cds. | | | | |
| DEFINITION | AF512998 | | | | |
| ACCESSION | AF512998.1 | GI:21314558 | | | |
| VERSION | | | | | |
| KEYWORDS | Danio rerio (zebrafish) | | | | |
| SOURCE | | | | | |
| ORGANISM | Danio rerio | | | | |
| REFERENCE | Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. | | | | |
| AUTHORS | Her, G.M., Yen, Y.H. and Wu, J.L. | | | | |
| TITLE | 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish | | | | |
| JOURNAL | Dev. Dyn. 227 (3), 347-356 (2003) | | | | |
| PUBMED | 12815620 | | | | |
| REFERENCE | 2 (bases 1 to 2960) | | | | |
| AUTHORS | Her, G.M. and Wu, J.-L. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chin-Yuan Road, Sec. 2, Taipei 115, Taiwan | | | | |
| FEATURES | Location/Qualifiers | | | | |
| SOURCE | 1..2960 | | | | |
| ORIGIN | /organism="Danio rerio" | | | | |
| mol_type | "genomic DNA" | | | | |
| db_xref | "taxon:7955" | | | | |
| product | "liver-type fatty acid binding protein" | | | | |
| note | "Lifebp; small cytosolic protein involved in lipid transport and metabolism" | | | | |
| codon_start | 1 | | | | |
| product | "liver-type fatty acid binding protein" | | | | |
| protein_id | "AAW47005.1" | | | | |
| db_xref | "GI:21314559" | | | | |
| translation | "MAFGSTWQVYAQENYEEFLRAISLPEVIAKLAKVPTIEIQNGSDPTITSKTPGKTV" | | | | |

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 23.3171 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaataacta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 6 | 20 | 100.0 | 480 | US-10-717-573-30 | Sequence 30, Appli |
| 7 | 20 | 100.0 | 2033 | US-10-677-254-3 | Sequence 3, Appli |
| 8 | 20 | 100.0 | 2033 | US-10-717-573-2 | Sequence 2, Appli |
| 9 | 20 | 100.0 | 2783 | US-10-717-573-2 | Sequence 2, Appli |
| 10 | 20 | 100.0 | 3003 | US-10-511-362-9 | Sequence 9, Appli |
| 11 | 18.4 | 92.0 | 13382 | US-10-612-594-4 | Sequence 4, Appli |
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| 16 | 17.4 | 87.0 | 635 | US-09-925-065A-563041 | Sequence 204324, |
| 17 | 17.4 | 87.0 | 1323 | US-09-925-065A-82927 | Sequence 82927, A |
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| C 24 | 16.8 | 84.0 | 642 | 4 | US-09-925-065A-340914 | Sequence 340914, |
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| C 26 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717970 | Sequence 717970, |
| C 27 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717971 | Sequence 717971, |
| C 28 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717972 | Sequence 717972, |
| C 29 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717973 | Sequence 717973, |
| C 30 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717974 | Sequence 717974, |
| C 31 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717975 | Sequence 717975, |
| C 32 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717976 | Sequence 717976, |
| C 33 | 16.8 | 84.0 | 3094 | 4 | US-09-925-065A-717977 | Sequence 717977, |
| C 34 | 16.8 | 84.0 | 5563 | 5 | US-10-136-734-26 | Sequence 26, Appli |
| C 35 | 16.8 | 84.0 | 8346 | 6 | US-10-240-453-202 | Sequence 202, Appli |
| C 36 | 16.8 | 84.0 | 96600 | 3 | US-09-997-722-85 | Sequence 85, Appli |
| C 37 | 16.4 | 82.0 | 700 | 4 | US-09-925-065A-688196 | Sequence 688196, |
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| C 42 | 15.8 | 79.0 | 401 | 3 | US-09-795-668-566 | Sequence 566, App |
| C 43 | 15.8 | 79.0 | 401 | 3 | US-09-795-668-567 | Sequence 567, App |
| C 44 | 15.8 | 79.0 | 401 | 3 | US-09-946-807-565 | Sequence 565, App |
| C 45 | 15.8 | 79.0 | 401 | 3 | US-09-946-807-566 | Sequence 566, App |

ALIGNMENTS

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RESULT 1
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; Sequence 9, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-9
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;
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Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TAGTTACCTTAATTACCTA 20
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RESULT 2
US-10-717-573-9
; Sequence 9, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 4.19294 Seconds
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Title: US-10-717-573-8

Perfect score: 21
Sequence: 1 tgaactgcctaatattaccctaa 21

Scoring table: IDENTITY_NUC
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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SUMMARIES

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| 6 | 16.8 | 80.0 | 601 | US-09-949-016-153876 | Sequence 153876, A |
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| 9 | 16.8 | 80.0 | 248968 | US-09-949-016-12614 | Sequence 12614, A |
| 10 | 16.8 | 80.0 | 250958 | US-09-949-016-16061 | Sequence 16061, A |
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| 12 | 16.4 | 78.1 | 102053 | US-09-949-016-13025 | Sequence 13025, A |
| 13 | 16.4 | 78.1 | 118999 | US-09-791-105B-32 | Sequence 32, Appl |
| 14 | 16.4 | 78.1 | 300598 | US-09-949-016-11868 | Sequence 11868, A |
| 15 | 16.4 | 78.1 | 302604 | US-09-949-016-14588 | Sequence 14588, A |
| 16 | 16.4 | 78.1 | 302602 | US-09-949-016-14589 | Sequence 14589, A |
| 17 | 16.4 | 78.1 | 308364 | US-09-949-016-11119 | Sequence 17119, A |
| 18 | 16.2 | 77.1 | 601 | US-09-949-016-141534 | Sequence 141534, A |
| 19 | 16.2 | 77.1 | 984 | US-09-792-024-21 | Sequence 21, Appl |
| 20 | 16.2 | 77.1 | 1060 | US-09-949-016-3687 | Sequence 3687, Ap |
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| 22 | 16.2 | 77.1 | 4598 | US-09-949-016-14343 | Sequence 14343, A |
| 23 | 16.2 | 77.1 | 39176 | US-09-949-016-17603 | Sequence 17603, A |
| 24 | 16.2 | 77.1 | 110266 | US-09-949-016-14913 | Sequence 14913, A |

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| 28 | 16.2 | 77.1 | 110266 | 3 | US-09-949-016-14917 | Sequence 14917, A |
| 29 | 16.2 | 77.1 | 110266 | 3 | US-09-949-016-14918 | Sequence 14918, A |
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| 38 | 16 | 76.2 | 209632 | 3 | US-09-949-002-802 | Sequence 802, App |
| 39 | 15.8 | 75.2 | 700 | 3 | US-09-735-271-961 | Sequence 961, App |
| 40 | 15.8 | 75.2 | 38261 | 3 | US-09-949-016-13802 | Sequence 13802, A |
| 41 | 15.8 | 75.2 | 221545 | 3 | US-09-949-016-13875 | Sequence 13875, A |
| 42 | 15.4 | 73.3 | 601 | 3 | US-09-949-016-135767 | Sequence 135767, A |
| 43 | 15.4 | 73.3 | 7127 | 3 | US-09-949-016-162532 | Sequence 162532, A |
| 44 | 15.4 | 73.3 | 7127 | 3 | US-09-949-016-162532 | Sequence 3, Appl |
| 45 | 15.4 | 73.3 | 24214 | 3 | US-09-949-016-15551 | Sequence 15551, A |

ALIGNMENTS

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RESULT 1
US-09-949-002-8712/c
; Sequence 8712, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8712
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-8712

Query Match      81.0%; Score 17; DB 3; Length 601;
Best Local Similarity 69.5%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TGACTTGCTTAATTACCT 19
       |:|||||
Db      302 TKTCTGCTTAATTACCT 284

RESULT 2
US-09-949-016-34841/c
; Sequence 34841, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 120.222 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hrc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_g882.*
10: gb_g882.*
11: gb_g883.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 21 | 100.0 | 253 | 3. BM025481 | BM025481 f879b01.y |
| 3 | 21 | 100.0 | 261 | 7. CN841194 | CN841194 AGENCOUKT |
| 4 | 21 | 100.0 | 297 | 6. CD606335 | CD606335 R2151A1P1 |
| 5 | 21 | 100.0 | 318 | 10. BX237207 | BX237207 Danio rer |
| 6 | 21 | 100.0 | 340 | 6. CD597232 | CD597232 RK103A2E0 |
| 7 | 21 | 100.0 | 340 | 6. CD601394 | CD601394 RK132A2F0 |
| 8 | 21 | 100.0 | 349 | 6. CD601336 | CD601336 RK132A1E0 |
| 9 | 21 | 100.0 | 350 | 6. CD592661 | CD592661 RK073A2E0 |
| 10 | 21 | 100.0 | 364 | 6. CD585167 | CD585167 RK029A4E0 |
| 11 | 21 | 100.0 | 379 | 10. BX163569 | BX163569 Danio rer |
| 12 | 21 | 100.0 | 404 | 1. AL731242 | AL731242 AL731242 |
| 13 | 21 | 100.0 | 412 | 11. DR388A2S | AL974517 Danio rer |
| 14 | 21 | 100.0 | 415 | 3. BM026582 | BM026582 f07b09.x |
| 15 | 21 | 100.0 | 421 | 3. BI983218 | BI983218 f045g04.x |
| 16 | 21 | 100.0 | 427 | 3. BM026426 | BM026426 f07b09.y |
| 17 | 21 | 100.0 | 431 | 1. AI878137 | AI878137 f057h07.y |
| 18 | 21 | 100.0 | 431 | 2. BG985624 | BG985624 5069 NICH |
| 19 | 21 | 100.0 | 435 | 1. AI878419 | AI878419 f057h07.x |
| 20 | 21 | 100.0 | 442 | 1. AI943080 | AI943080 f084a05.x |
| 21 | 21 | 100.0 | 444 | 3. BM155502 | BM155502 f06f01.y |
| 22 | 21 | 100.0 | 446 | 1. AL910060 | AL910060 AL910060 |

| | | | | | |
|----|----|-------|-----|--------------|--------------------|
| 23 | 21 | 100.0 | 453 | 3. BI430094 | BI430094 f087h10.x |
| 24 | 21 | 100.0 | 456 | 3. BI476314 | BI476314 f026e07.x |
| 25 | 21 | 100.0 | 462 | 1. AI667066 | AI667066 f037c02.x |
| 26 | 21 | 100.0 | 463 | 1. AI396940 | AI396940 f07e03.x |
| 27 | 21 | 100.0 | 464 | 2. BE201284 | BE201284 f089c10.y |
| 28 | 21 | 100.0 | 466 | 3. BI428752 | BI428752 f073a01.x |
| 29 | 21 | 100.0 | 468 | 6. CB352105 | CB352105 f0001-P00 |
| 30 | 21 | 100.0 | 477 | 1. AI545438 | AI545438 f081c03.x |
| 31 | 21 | 100.0 | 483 | 3. BM071181 | BM071181 f03h04.x |
| 32 | 21 | 100.0 | 489 | 10. BX167558 | BI67558 Danio rer |
| 33 | 21 | 100.0 | 492 | 1. AI878707 | AI878707 f064g04.x |
| 34 | 21 | 100.0 | 498 | 1. AM826633 | AM826633 f055a12.x |
| 35 | 21 | 100.0 | 504 | 11. DR35716S | AL979317 Danio rer |
| 36 | 21 | 100.0 | 505 | 3. BI840860 | BI840860 f039f10.x |
| 37 | 21 | 100.0 | 514 | 11. DR4609T | AL982918 Danio rer |
| 38 | 21 | 100.0 | 518 | 3. BI880089 | BI880089 f069f06.x |
| 39 | 21 | 100.0 | 520 | 1. AL928427 | AL928427 AL928427 |
| 40 | 21 | 100.0 | 523 | 3. BM531885 | BM531885 f032c11.y |
| 41 | 21 | 100.0 | 523 | 6. CB359375 | CB359375 f0001-P00 |
| 42 | 21 | 100.0 | 530 | 3. BI430060 | BI430060 f087h10.y |
| 43 | 21 | 100.0 | 536 | 3. BI428231 | BI428231 f076c09.x |
| 44 | 21 | 100.0 | 539 | 7. CR928386 | CR928386 CR928386 |
| 45 | 21 | 100.0 | 542 | 3. BI325511 | BI325511 f039b08.x |

ALIGNMENTS

RESULT 1
LOCUS BX124567 169 bp DNA linear GSS 13-MAR-2003
DEFINITION Danio rerio genomic clone DKEX-65A3, genomic survey sequence.
ACCESSION BX124567
VERSION BX124567.1 GI:27955505
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

REFERENCE

1 (bases 1 to 169)
Humphray, S.J., Huckle, E. and Durham, J.L.
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphraysanger.ac.uk Unpublished

COMMENT

This sequence was generated from the 5' end of BAC 65A3. 65A3 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source
1..169
Location/Qualifiers
1..169
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-65A3"
/tissue_type="Testis"
/note="vector pindigBAC-536"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 169;
Best Local Similarity 100.0%; Pred. No. 7.8; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGACTTGCTTAATACCTTA 21

76 TGACTTGCTTAATACCTTA 96

RESULT 2

BM025481/c 253 bp mRNA linear EST 30-OCT-2001
LOCUS f879b01.y1 zebrafish SUD day 8 fin regeneration Danio rerio cDNA
DEFINITION

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 17.1875 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-8

Perfect score: 21

Sequence: 1 tgacttgctattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003d:*
11: geneseqn2003e:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 21 | 100.0 | 21 | 13 | ADT08249 |
| 2 | 21 | 100.0 | 21 | 13 | ADT89057 |
| 3 | 21 | 100.0 | 435 | 13 | ADT08242 |
| 4 | 21 | 100.0 | 435 | 13 | ADT89050 |
| 5 | 21 | 100.0 | 480 | 13 | ADT08271 |
| 6 | 21 | 100.0 | 480 | 13 | ADT89079 |
| 7 | 21 | 100.0 | 2033 | 13 | ADT08244 |
| 8 | 21 | 100.0 | 2033 | 13 | ADT89052 |
| 9 | 21 | 100.0 | 2783 | 13 | ADT08243 |
| 10 | 21 | 100.0 | 2783 | 13 | ADT89051 |
| 11 | 21 | 100.0 | 2960 | 13 | ADT89080 |
| 12 | 19.4 | 92.4 | 7495 | 13 | ADT890815 |
| 13 | 19.4 | 92.4 | 7508 | 13 | ADT890814 |
| 14 | 19.4 | 92.4 | 71843 | 8 | ACC79619 |
| 15 | 17.8 | 84.8 | 13382 | 14 | ADT44488 |
| 16 | 17.8 | 84.8 | 78064 | 13 | ADT17402 |
| 17 | 16.8 | 80.0 | 78064 | 13 | ADT17402 |
| 18 | 16.4 | 78.1 | 5000 | 4 | AA514506 |
| 19 | 16.4 | 78.1 | 6070 | 6 | ABL33679 |

| | | | | | | | |
|---|----|------|------|-------|----|----------|--------------------|
| c | 20 | 16.4 | 78.1 | 6070 | 6 | ABL34579 | Ab134579 Human met |
| c | 21 | 16.4 | 78.1 | 6070 | 6 | ABL70372 | Ab170372 Chemical1 |
| c | 22 | 16.4 | 78.1 | 6070 | 6 | ABO67130 | Ab067130 Human ang |
| c | 23 | 16.4 | 78.1 | 6070 | 7 | ADS99840 | Ad999840 Complem |
| c | 24 | 16.4 | 78.1 | 6197 | 6 | ABN80256 | Abn80256 Human che |
| c | 25 | 16.4 | 78.1 | 7049 | 6 | ABN32156 | Ab132156 Human imm |
| c | 26 | 16.4 | 78.1 | 7049 | 6 | ABL54305 | Ab154305 Chemical1 |
| c | 27 | 16.4 | 78.1 | 10716 | 6 | ABL33418 | Ab133418 Human imm |
| c | 28 | 16.4 | 78.1 | 33053 | 6 | ABO67006 | Ab067006 Human ang |
| c | 29 | 16.4 | 78.1 | 34548 | 6 | ABL70604 | Ab170604 Chemical1 |
| c | 30 | 16.4 | 78.1 | 37973 | 6 | ABL34196 | Ab134196 Human imm |
| c | 31 | 16.4 | 78.1 | 73334 | 6 | ABL34125 | Ab134125 Human imm |
| c | 32 | 16.4 | 78.1 | 73334 | 6 | ABL92319 | Ab192319 Chemical1 |
| c | 33 | 16.4 | 78.1 | 76798 | 6 | ABN97454 | Abn97454 Gene #395 |
| c | 34 | 16.4 | 78.1 | 76798 | 14 | ADT06902 | Adt06902 Cyclin-de |
| c | 35 | 16.4 | 78.1 | 83391 | 6 | ABO67093 | Ab067093 Human ang |
| c | 36 | 16.2 | 77.1 | 401 | 9 | ACH48896 | Ach48896 Human leu |
| c | 37 | 16.2 | 77.1 | 431 | 5 | AA583152 | AA583152 DNA encod |
| c | 38 | 16.2 | 77.1 | 431 | 12 | ADO40991 | Ado40991 Human cDN |
| c | 39 | 16.2 | 77.1 | 441 | 4 | ABA89222 | Ab89222 Escherich |
| c | 40 | 16.2 | 77.1 | 501 | 12 | ACH74075 | Ach74075 Human gen |
| c | 41 | 16.2 | 77.1 | 512 | 12 | ACH71469 | Ach71469 Human gen |
| c | 42 | 16.2 | 77.1 | 559 | 9 | ACH16166 | Ach16166 Human adu |
| c | 43 | 16.2 | 77.1 | 587 | 4 | AA525471 | AA525471 Human ova |
| c | 44 | 16.2 | 77.1 | 621 | 3 | AA05868 | AA05868 Group B S |
| c | 45 | 16.2 | 77.1 | 636 | 13 | ACN51439 | Acn51439 Cotton an |

ALIGNMENTS

RESULT 1
ADT08249
ID ADT08249 standard; DNA, 21 BP.

XX ADT08249;

DT 13-JAN-2005 (first entry)

XX Zebrafish L-FABP upstream region PDX1 binding site.

XX Zebrafish; ds; liver fatty acid binding protein; L-FABP;

KW liver regulatory element; LR; transgenic; HPH(1); HPH(2); HNF-1alpha;

KM HNF-3 beta; PDX1; PDX; green fluorescent protein; GFP;

KW liver development; liver disease; liver necrosis; liver cancer.

OS Danio rerio.

XX US2004209833-A1.

PN 21-NOV-2003; 2003US-00717573.

XX 21-OCT-2004.

XX 21-NOV-2003; 2003US-0463035P.

XX 27-MAY-2003; 2003US-0473210P.

XX (WUJG/) WU J. M.

XX (HERG/) HER G. M.

XX Wu J, Her GM;

XX WPI; 2004-765481/75.

XX New isolated polynucleotide useful for generating transgenic fish such as

PT zebrafish, comprises liver-specific expression control sequence that

PT modulates expression of vertebrate liver fatty acid binding protein.

XX Claim 5; SEQ ID NO 8; 40bp; English.

XX The invention relates to an isolated polynucleotide comprising a liver-

CC specific expression control sequence (LR) which modulates expression of a

CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 / Search time 124.933 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-8

Perfect score: 21
Sequence: 1 Tgactgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBml:.*
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15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 100.0 | 1650 | BC095039 | Danio rer |
| 3 | 100.0 | 2065 | BC076409 | Danio rer |
| 4 | 100.0 | 2191 | BC076409 | Danio rer |
| 5 | 100.0 | 2635 | BC076409 | Danio rer |
| 6 | 100.0 | 2905 | BC092170 | Danio rer |
| 7 | 100.0 | 2960 | AF512998 | Danio rer |
| 8 | 100.0 | 16353 | CR352254 | zebrafish |
| 9 | 100.0 | 23743 | CR376835 | zebrafish |
| 10 | 100.0 | 23988 | CR762446_5 | zebrafish |
| 11 | 100.0 | 31940 | CR385072 | zebrafish |
| 12 | 100.0 | 32786 | CR571835 | zebrafish |
| 13 | 100.0 | 38062 | CR759876 | Danio rer |
| 14 | 100.0 | 39233 | CR388362 | zebrafish |
| 15 | 100.0 | 39267 | CR388362 | zebrafish |
| 16 | 100.0 | 41950 | CR555959 | zebrafish |
| 17 | 100.0 | 42660 | CR549278 | zebrafish |
| 18 | 100.0 | 43563 | CR556724 | zebrafish |
| | | | BX470103 | zebrafish |

| | | | | |
|----|-------|-------|------------|-----------|
| 19 | 100.0 | 44797 | CR753881 | zebrafish |
| 20 | 100.0 | 47275 | BX897669 | zebrafish |
| 21 | 100.0 | 47333 | AL928934 | zebrafish |
| 22 | 100.0 | 47442 | AC146465 | Danio rer |
| 23 | 100.0 | 49875 | BX510921 | zebrafish |
| 24 | 100.0 | 50111 | CR762393 | zebrafish |
| 25 | 100.0 | 50895 | AL732386 | zebrafish |
| 26 | 100.0 | 51808 | AC104683 | Danio rer |
| 27 | 100.0 | 52909 | CR753895_3 | zebrafish |
| 28 | 100.0 | 53370 | AC144825 | Danio rer |
| 29 | 100.0 | 53530 | CR388040 | zebrafish |
| 30 | 100.0 | 54100 | CR48730 | Danio rer |
| 31 | 100.0 | 57059 | CR450822 | zebrafish |
| 32 | 100.0 | 58039 | CR759821 | zebrafish |
| 33 | 100.0 | 58124 | CR937028 | zebrafish |
| 34 | 100.0 | 58638 | BX248388 | zebrafish |
| 35 | 100.0 | 60081 | BX088711_3 | zebrafish |
| 36 | 100.0 | 61341 | BX666063 | zebrafish |
| 37 | 100.0 | 62252 | BX322549 | zebrafish |
| 38 | 100.0 | 62994 | BX255886 | zebrafish |
| 39 | 100.0 | 63779 | AL845322 | zebrafish |
| 40 | 100.0 | 64422 | BX897748 | zebrafish |
| 41 | 100.0 | 67061 | CR354609_3 | zebrafish |
| 42 | 100.0 | 67355 | BX649395_3 | zebrafish |
| 43 | 100.0 | 67817 | BX950227 | zebrafish |
| 44 | 100.0 | 69669 | AL591664 | zebrafish |
| 45 | 100.0 | 70420 | BX470074 | zebrafish |

ALIGNMENTS

BC095039 1579 bp mRNA linear VRT 06-JUN-2005
Danio rerio zgc:109899, mRNA (CDNA clone MGC:109899 IMAGE:722575), complete cde.
BC095039.1 GI:63101752
MGC.
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1579)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Burow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Stappleton, M., Marusina, K., Farmer, A.A., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulhally, S.J., Bosak, S.A., McGowan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wootley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.R., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherbakov, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalske, U., Smallos, D.E., Schmeck, A., Schein, J.E., Jones, S.J., and Warr, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1579)
NIM MGC Project
Direct Submission

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 18.6545 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-8

Perfect score: 21

Sequence: 1 TGACTTGCTGAATCCTAA 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues 18527782

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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| 1 | 17.8 | 84.8 | 3417 | 8 | US-10-750-185-33312, A |
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| 16 | 17.4 | 82.9 | 1076 | 6 | US-09-925-065A-699655, A |
| 17 | 17.4 | 82.9 | 1076 | 6 | US-09-925-065A-699655, A |
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| 20 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
| 21 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
| 22 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
| 23 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
| 24 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
| 25 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
| 26 | 16.4 | 78.1 | 554 | 6 | US-09-925-065A-552951, A |
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| 28 | 16.2 | 77.1 | 522 | 6 | US-09-925-065A-551205, A |
| 29 | 16.2 | 77.1 | 522 | 6 | US-09-925-065A-551205, A |
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| 31 | 16.2 | 77.1 | 522 | 6 | US-09-925-065A-551205, A |
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ALIGNMENTS

RESULT 1
US-10-750-185-33312, Application US/10750185
Sequence 33312, A
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33312
LENGTH: 3417
TYPE: DNA
ORGANISM: Bovine 19866880478621
US-10-750-185-33312
Query Match 84.8%, Score 17.8, DB 8; Length 3417;
Best Local Similarity 90.5%, Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TGACTTGCTGAATCCTAA 21
DB 3116 TGACTTGCTGAATCCTAA 3136
RESULT 2
US-10-750-623-33312, Application US/10750623
Sequence 33312, A
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 24.483 Seconds
(Without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-8

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Scoring table: IDENTITY NUC
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 11 | 19.4 | 92.4 | 7495 | 7 | US-10-742-828-5 |
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| 14 | 17.8 | 84.8 | 13382 | 8 | US-10-613-594-4 |
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| 16 | 17.4 | 82.9 | 1076 | 4 | US-09-925-065A-699655 |
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| 18 | 17 | 81.0 | 561 | 4 | US-09-925-065A-346440 |
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| 24 | 16.8 | 80.0 | 583 | 4 | US-09-925-065A-375086 | Sequence 375086, A |
| 25 | 16.8 | 80.0 | 317129 | 8 | US-10-741-600-17765 | Sequence 17765, A |
| 26 | 16.4 | 78.1 | 554 | 4 | US-09-925-065A-652951 | Sequence 652951, A |
| 27 | 16.4 | 78.1 | 644 | 4 | US-09-925-065A-730267 | Sequence 730267, A |
| 28 | 16.4 | 78.1 | 697 | 5 | US-10-027-632-43982 | Sequence 43982, A |
| 29 | 16.4 | 78.1 | 697 | 6 | US-10-027-632-43982 | Sequence 43982, A |
| 30 | 16.4 | 78.1 | 1694 | 4 | US-09-925-065A-90595 | Sequence 90595, A |
| 31 | 16.4 | 78.1 | 2292 | 4 | US-09-925-065A-549598 | Sequence 549598, A |
| 32 | 16.4 | 78.1 | 5000 | 2 | US-09-791-105-2 | Sequence 2, Appl1 |
| 33 | 16.4 | 78.1 | 6070 | 6 | US-10-311-455-1652 | Sequence 1652, Ap |
| 34 | 16.4 | 78.1 | 6070 | 6 | US-10-240-485-132 | Sequence 132, App |
| 35 | 16.4 | 78.1 | 6070 | 7 | US-10-433-793-160 | Sequence 160, App |
| 36 | 16.4 | 78.1 | 7049 | 6 | US-10-311-455-1129 | Sequence 129, App |
| 37 | 16.4 | 78.1 | 7049 | 6 | US-10-240-452-5 | Sequence 5, Appl1 |
| 38 | 16.4 | 78.1 | 10716 | 6 | US-10-311-455-1391 | Sequence 1391, Ap |
| 39 | 16.4 | 78.1 | 33053 | 7 | US-10-433-793-36 | Sequence 36, Appl |
| 40 | 16.4 | 78.1 | 37973 | 6 | US-10-311-455-2169 | Sequence 2169, Ap |
| 41 | 16.4 | 78.1 | 73334 | 7 | US-10-311-455-2098 | Sequence 2098, Ap |
| 42 | 16.4 | 78.1 | 73334 | 7 | US-10-240-589C-128 | Sequence 128, App |
| 43 | 16.4 | 78.1 | 76798 | 3 | US-09-880-107-3949 | Sequence 3949, Ap |
| 44 | 16.4 | 78.1 | 83391 | 7 | US-10-433-793-123 | Sequence 123, App |
| 45 | 16.4 | 78.1 | 2140405 | 5 | US-10-027-632-76212 | Sequence 76212, A |

ALIGNMENTS

RESULT 1
US-10-677-254-8
Sequence 8, Application US/10677254
Publication No. US20040209279A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
FILE REFERENCE: 33151-188802
CURRENT APPLICATION NUMBER: US/10/677,254
CURRENT FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 21
TYPE: DNA
ORGANISM: Danio rerio
US-10-677-254-8
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Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 Tgacttgccctaatcaccctaa 21
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US-10-717-573-8
Sequence 8, Application US/10717573
Publication No. US20040209833A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
FILE REFERENCE: 33151-188802
CURRENT APPLICATION NUMBER: US/10/717,573
CURRENT FILING DATE: 2003-11-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 21
TYPE: DNA

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 3.99328 Seconds
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Title: US-10-717-573-7

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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 18.4 | 92.0 | 360 | US-08-781-986A-3007 | Sequence 3007, Ap |
| 3 | 18.4 | 92.0 | 2854 | US-08-936-165A-66 | Sequence 66, Appl |
| 4 | 18.4 | 92.0 | 3774 | US-08-956-171E-660 | Sequence 660, App |
| 5 | 18.4 | 92.0 | 3774 | US-08-781-986A-660 | Sequence 660, App |
| 6 | 17.4 | 87.0 | 360 | US-09-270-767-8176 | Sequence 8176, Ap |
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| 8 | 17.4 | 87.0 | 601 | US-09-949-016-120222 | Sequence 120222, A |
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| 10 | 17.4 | 87.0 | 133063 | US-09-949-016-15613 | Sequence 15613, A |
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| 13 | 16.8 | 84.0 | 2641 | US-10-104-047-1176 | Sequence 1176, Ap |
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| 16 | 16.8 | 84.0 | 3348 | US-09-710-279-3732 | Sequence 3732, Ap |
| 17 | 16.8 | 84.0 | 3417 | US-09-710-279-4318 | Sequence 4318, Ap |
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| 23 | 16.8 | 84.0 | 22914 | US-09-949-016-16270 | Sequence 16270, A |
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| 25 | 16.8 | 84.0 | 46920 | US-09-949-016-11954 | Sequence 11954, A |
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| 28 | 16.8 | 84.0 | 54576 | US-09-949-016-15955 | Sequence 15955, A |
| 29 | 16.8 | 84.0 | 60593 | US-09-949-016-13779 | Sequence 13779, A |
| 30 | 16.8 | 84.0 | 76810 | US-09-949-016-12528 | Sequence 12528, A |
| 31 | 16.8 | 84.0 | 83462 | US-09-949-016-12211 | Sequence 12211, A |
| 32 | 16.8 | 84.0 | 85368 | US-09-949-016-12502 | Sequence 12502, A |
| 33 | 16.8 | 84.0 | 157032 | US-09-949-016-12928 | Sequence 12928, A |
| 34 | 16.8 | 84.0 | 194537 | US-09-949-016-12740 | Sequence 12740, A |
| 35 | 16.8 | 84.0 | 201529 | US-09-949-016-12741 | Sequence 12741, A |
| 36 | 16.8 | 84.0 | 373182 | US-09-949-016-17371 | Sequence 17371, A |
| 37 | 16.8 | 84.0 | 373694 | US-09-949-016-12062 | Sequence 12062, A |
| 38 | 16.8 | 84.0 | 1664976 | US-08-916-421B-1 | Sequence 1, Appli |
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| 40 | 16.8 | 84.0 | 1664976 | US-09-692-570-1 | Sequence 1, Appli |
| 41 | 16.8 | 84.0 | 1664976 | US-09-692-570-1 | Sequence 1, Appli |
| 42 | 16.4 | 82.0 | 433 | US-09-270-767-4014 | Sequence 4014, Ap |
| 43 | 16.4 | 82.0 | 433 | US-09-270-767-15296 | Sequence 15296, A |
| 44 | 16.4 | 82.0 | 601 | US-09-949-016-85309 | Sequence 85309, A |
| 45 | 16.4 | 82.0 | 601 | US-09-949-016-206794 | Sequence 206794, A |

ALIGNMENTS

RESULT 1
US-08-956-171E-3007/c
Sequence 3007, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gil H. Choi
Craig S. Dillon
Steven A. Rosen
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3007:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 114.498 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attttaagcaacaacttaa 20

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Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 36 | 18.4 | 92.0 | 579 | 3 | BM406069 |
| C 37 | 18.4 | 92.0 | 580 | 10 | CM959294 |
| C 38 | 18.4 | 92.0 | 626 | 11 | BK420255 |
| C 39 | 18.4 | 92.0 | 636 | 11 | DR43G11T |
| C 40 | 18.4 | 92.0 | 640 | 7 | CO353502 |
| C 41 | 18.4 | 92.0 | 659 | 9 | AZ349621 |
| C 42 | 18.4 | 92.0 | 673 | 7 | CK680521 |
| C 43 | 18.4 | 92.0 | 687 | 10 | BK197109 |
| C 44 | 18.4 | 92.0 | 699 | 9 | AZ416632 |
| C 45 | 18.4 | 92.0 | 706 | 10 | BK208190 |

ALIGNMENTS

RESULT 1
LOCUS B628666
DEFINITION 1h61e11.g1 WGS-Sbicolorf (DH5a methyl filtered) Sorghum bicolor
ACCESSION B628666
VERSION B628666.1 GI:27780751
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 606)
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zlatavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A. Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: 1h61 row: e column: 11
Seq primer: -21M3univRev
Class: shotgun
High quality sequence stop: 606.
Location/Qualifiers
1..606
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="1h61e11"
/lab_host="DH5a"
/clone_1lb="WGS-Sbicolorf (DH5a methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I, and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 16.3691 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-7

Perfect score: 20

Sequence: 1 attcaagcaacaactaa 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*
14: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 20 | 100.0 | 20 | 13 | ADT08248 |
| 2 | 20 | 100.0 | 20 | 13 | ADT89056 |
| 3 | 20 | 100.0 | 435 | 13 | ADT08242 |
| 4 | 20 | 100.0 | 435 | 13 | ADT89050 |
| 5 | 20 | 100.0 | 480 | 13 | ADT08271 |
| 6 | 20 | 100.0 | 480 | 13 | ADT89079 |
| 7 | 20 | 100.0 | 2033 | 13 | ADT08244 |
| 8 | 20 | 100.0 | 2033 | 13 | ADT89052 |
| 9 | 20 | 100.0 | 2766 | 6 | ABZ70273 |
| 10 | 20 | 100.0 | 2783 | 13 | ADT08243 |
| 11 | 20 | 100.0 | 2783 | 13 | ADT89051 |
| 12 | 20 | 100.0 | 2960 | 13 | ADT89080 |
| 13 | 20 | 100.0 | 360 | 2 | AAV77318 |
| 14 | 18.4 | 92.0 | 1485 | 4 | AA552127 |
| 15 | 18.4 | 92.0 | 1539 | 4 | AA55190 |
| 16 | 18.4 | 92.0 | 1539 | 4 | AA54952 |
| 17 | 18.4 | 92.0 | 1539 | 8 | ACR20111 |
| 18 | 18.4 | 92.0 | 1539 | 8 | ACF74068 |
| 19 | 18.4 | 92.0 | 2854 | 2 | AAV53366 |

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|---|----|------|------|--------|----|----------|---------------------|
| C | 20 | 18.4 | 92.0 | 3774 | 2 | AAV74971 | AAV74971 Staphyloc |
| C | 21 | 18 | 90.0 | 85548 | 13 | ADV34999 | Adv34999 Murine CD |
| C | 22 | 17.4 | 87.0 | 473 | 6 | ABA90463 | AbA90463 Drosophill |
| C | 23 | 17.4 | 87.0 | 473 | 6 | ABA90465 | AbA90465 Drosophill |
| C | 24 | 17.4 | 87.0 | 511 | 12 | AD085873 | Ad085873 Exon 3 of |
| C | 25 | 17.4 | 87.0 | 539 | 6 | ABA90464 | AbA90464 Drosophill |
| C | 26 | 17.4 | 87.0 | 906 | 4 | AAK80378 | AAK80378 Human Imm |
| C | 27 | 17.4 | 87.0 | 906 | 4 | AAK74454 | AAK74454 Human Imm |
| C | 28 | 17.4 | 87.0 | 1933 | 6 | ABZ57726 | AbZ57726 Human NAD |
| C | 29 | 17.4 | 87.0 | 3516 | 4 | ABL29338 | AbL29338 Drosophill |
| C | 30 | 17.4 | 87.0 | 3907 | 4 | ABL29360 | AbL29360 Drosophill |
| C | 31 | 17.4 | 87.0 | 33632 | 4 | ABL29040 | AbL29040 Drosophill |
| C | 32 | 17.4 | 87.0 | 37322 | 6 | ABL1996 | AbL1996 Colon ade |
| C | 33 | 17.4 | 87.0 | 104000 | 8 | AD57669 | Ad57669 Human pho |
| C | 34 | 17 | 85.0 | 702 | 8 | ACA30280 | AcA30280 Prokaryot |
| C | 35 | 17 | 85.0 | 712 | 2 | AAK25080 | AAK25080 Potato tu |
| C | 36 | 17 | 85.0 | 10200 | 4 | AAK7727 | AAK7727 Human Imm |
| C | 37 | 17 | 85.0 | 154902 | 6 | ABQ88198 | AbQ88198 Human ost |
| C | 38 | 16.8 | 84.0 | 107 | 2 | AAQ77341 | AAQ77341 Human gen |
| C | 39 | 16.8 | 84.0 | 141 | 13 | ADS04162 | AdS04162 Staphyloc |
| C | 40 | 16.8 | 84.0 | 165 | 13 | ADS04074 | AdS04074 Staphyloc |
| C | 41 | 16.8 | 84.0 | 307 | 3 | AAFL8364 | AAFL8364 Lung Canc |
| C | 42 | 16.8 | 84.0 | 462 | 4 | AAK56918 | AAK56918 Human Imm |
| C | 43 | 16.8 | 84.0 | 534 | 5 | ABV52288 | AbV52288 Human pro |
| C | 44 | 16.8 | 84.0 | 549 | 3 | ACG3993 | AcG3993 Cat flea |
| C | 45 | 16.8 | 84.0 | 549 | 3 | ACG4850 | AcG4850 Cat flea |

ALIGNMENTS

| | | |
|----------|---|--------------------------------|
| RESULT 1 | ADT08248 | ADT08248 standard; DNA; 20 BP. |
| ID | ADT08248 | |
| XX | 13-JUN-2005 (first entry) | |
| XX | Zebrafish L-FABP upstream region HNF-3beta binding site. | |
| XX | Zebrafish; ds; liver fatty acid binding protein; L-FABP; | |
| KM | liver regulatory element; LR; transgenic; HNF(1); HNF(2); HNF-1alpha; | |
| KM | HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP; | |
| KM | liver development; liver disease; liver necrosis; liver cancer. | |
| XX | Danio rerio. | |
| OS | | |
| XX | US2004209833-A1. | |
| PN | | |
| XX | 21-OCT-2004. | |
| PD | | |
| XX | 21-NOV-2003; 2003US-00717573. | |
| PF | | |
| XX | 16-APR-2003; 2003US-0463035P. | |
| PR | 27-MAY-2003; 2003US-0473210P. | |
| XX | (WUJG/) WU J. | |
| PA | (HERG/) HER G M. | |
| XX | | |
| XX | Wu J, Her GM; | |
| XX | WPI; 2004-765481/75. | |
| DR | | |
| XX | New isolated polynucleotide useful for generating transgenic fish such as | |
| PT | zebrafish, comprises liver-specific expression control sequence that | |
| PT | modulates expression of vertebrate liver fatty acid binding protein. | |
| XX | Claim 4; SEQ ID NO 7; 40bp; English. | |
| PS | | |
| XX | The invention relates to an isolated polynucleotide comprising a liver- | |
| CC | specific expression control sequence (Lr) which modulates expression of a | |
| CC | vertebrate liver fatty acid binding protein (L-FABP). Also included are a | |

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OM nucleic - nucleic search, using bw model

Run on: April 1, 2006, 05:44:25 ; Search time 118.984 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-7

Perfect score: 20

Sequence: 1 atttaagcaacaattaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBml:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 20 | 100.0 | 2960 | 5 | AF512998 Danto rer |
| 2 | 20 | 100.0 | 60709 | 14 | AC107923 Homo sapi |
| 3 | 20 | 100.0 | 121952 | 14 | AC151673 Medicago |
| 4 | 20 | 100.0 | 121953 | 15 | AC125481 Medicago |
| 5 | 20 | 100.0 | 142257 | 5 | BX005151 Zebrafish |
| 6 | 20 | 100.0 | 151057 | 8 | AC019198 Homo sapi |
| 7 | 20 | 100.0 | 151397 | 14 | CR792430 Danto rer |
| 8 | 20 | 100.0 | 154065 | 5 | CR854838 Zebrafish |
| 9 | 20 | 100.0 | 156578 | 14 | CR786577 Danto rer |
| 10 | 20 | 100.0 | 159188 | 5 | CR381658 Zebrafish |
| 11 | 20 | 100.0 | 168663 | 8 | AL354815 Human DNA |
| 12 | 20 | 100.0 | 176047 | 9 | AC102338 Mus muscu |
| 13 | 20 | 100.0 | 178271 | 5 | CR293507 Zebrafish |
| 14 | 20 | 100.0 | 184243 | 5 | AC102296 Mus muscu |
| 15 | 19 | 95.0 | 169 | 10 | AB150316 Homo sapi |
| 16 | 19 | 95.0 | 244 | 15 | AY018859 Homo sapi |
| 17 | 19 | 95.0 | 58009 | 14 | AC087383 Homo sapi |
| 18 | 19 | 95.0 | 107758 | 14 | CR925770 Danto rer |

| | | | | | | |
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| c 19 | 19 | 95.0 | 110000 | 15 | AP008211_033 | Continuation (34 0 |
| c 20 | 19 | 95.0 | 151235 | 8 | AC090936 | AC090936 Homo sapi |
| c 21 | 19 | 95.0 | 159577 | 14 | AC080060 | AC080060 Homo sapi |
| c 22 | 19 | 95.0 | 160949 | 14 | AC139622 | AC139622 Danto rer |
| c 23 | 19 | 95.0 | 162088 | 14 | AC069472 | AC069472 Homo sapi |
| c 24 | 19 | 95.0 | 177153 | 15 | AC119288 | AC119288 Oryza sat |
| c 25 | 19 | 95.0 | 221511 | 5 | CR391905 | CR391905 Zebrafish |
| c 26 | 19 | 95.0 | 233137 | 14 | AC094489 | AC094489 Rattus no |
| c 27 | 19 | 95.0 | 239843 | 14 | AC115518 | AC115518 Rattus no |
| c 28 | 18.4 | 92.0 | 360 | 6 | AR356889 | AR356889 Sequence |
| c 29 | 18.4 | 92.0 | 360 | 6 | AR384445 | AR384445 Sequence |
| c 30 | 18.4 | 92.0 | 791 | 10 | BV641492 | BV641492 S215P6173 |
| c 31 | 18.4 | 92.0 | 1539 | 6 | AX620532 | AX620532 Sequence |
| c 32 | 18.4 | 92.0 | 1605 | 5 | BC095656 | BC095656 Danto rer |
| c 33 | 18.4 | 92.0 | 1821 | 2 | AK114237 | AK114237 Clona int |
| c 34 | 18.4 | 92.0 | 2854 | 6 | AR194517 | AR194517 Sequence |
| c 35 | 18.4 | 92.0 | 3774 | 6 | AR354542 | AR354542 Sequence |
| c 36 | 18.4 | 92.0 | 3774 | 6 | AR356098 | AR356098 Sequence |
| c 37 | 18.4 | 92.0 | 38279 | 8 | AC127900 | AC127900 Homo sapi |
| c 38 | 18.4 | 92.0 | 42644 | 5 | CR627499 | CR627499 Zebrafish |
| c 39 | 18.4 | 92.0 | 60218 | 5 | CR387987 | CR387987 Zebrafish |
| c 40 | 18.4 | 92.0 | 64183 | 14 | AC164395 | AC164395 Medicago |
| c 41 | 18.4 | 92.0 | 65750 | 8 | AC092542 | AC092542 Homo sapi |
| c 42 | 18.4 | 92.0 | 66694 | 5 | BX908791 | BX908791 Zebrafish |
| c 43 | 18.4 | 92.0 | 77143 | 5 | BX927094 | BX927094 Zebrafish |
| c 44 | 18.4 | 92.0 | 80171 | 5 | BX544872 | BX544872 Zebrafish |
| c 45 | 18.4 | 92.0 | 80589 | 5 | BX470257 | BX470257 Zebrafish |

ALIGNMENTS

| | | | | | |
|------------|--|-------------|-----|--------|-----------------|
| RESULT 1 | AF512998 | 2960 bp | DNA | linear | VRT 10-JUN-2003 |
| LOCUS | Danto rerio liver-type fatty acid binding protein gene, partial cde. | | | | |
| DEFINITION | Danto rerio liver-type fatty acid binding protein gene, partial cde. | | | | |
| ACCESSION | AF512998 | | | | |
| VERSION | AF512998.1 | GI:21314558 | | | |
| KEYWORDS | | | | | |
| SOURCE | Danto rerio (zebrafish) | | | | |
| ORGANISM | Danto rerio | | | | |
| REFERENCE | Her, G.M., Yeh, Y.H. and Wu, J.L. 1995. A 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish Dev. Dyn. 227 (3), 347-356 (2003) | | | | |
| AUTHORS | Her, G.M., Yeh, Y.H. and Wu, J.L. | | | | |
| TITLE | 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish | | | | |
| JOURNAL | Dev. Dyn. 227 (3), 347-356 (2003) | | | | |
| PUBMED | 12815620 | | | | |
| REFERENCE | 2 (bases 1 to 2960) | | | | |
| AUTHORS | Her, G.M. and Wu, J.-L. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan | | | | |
| FEATURES | Location/Qualifiers | | | | |
| SOURCE | 1..2960 | | | | |
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| | /product="liver-type fatty acid binding protein" | | | | |
| | /note="Lfabp; small cytosolic protein involved in lipid transport and metabolism" | | | | |
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| | /product="liver-type fatty acid binding protein" | | | | |
| | /protein_id="AA047005.1" | | | | |
| | /db_xref="GI:21314559" | | | | |
| | /translation="MAFGSTWQVYAOENYEFRAISLPREVIKADVAPVETIQNGSDPTIRSKTPGKTV" | | | | |

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 17.7662 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attcaagaacaacaaattaa 20

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New: *
1: /SIDSS/ptcodata/2/pubpna/US08_NEW_PUB_seq.*
2: /SIDSS/ptcodata/2/pubpna/US06_NEW_PUB_seq.*
3: /SIDSS/ptcodata/2/pubpna/US07_NEW_PUB_seq.*
4: /SIDSS/ptcodata/2/pubpna/PCRT_NEW_PUB_seq.*
5: /SIDSS/ptcodata/2/pubpna/US09_NEW_PUB_seq.*
6: /SIDSS/ptcodata/2/pubpna/US10_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| C 1 | 18.4 | 92.0 | 529 | 10 US-10-301-480-486528 | Sequence 486528, |
| C 2 | 18.4 | 92.0 | 529 | 10 US-10-301-480-109937 | Sequence 109937, |
| C 3 | 18.4 | 92.0 | 531 | 6 US-09-925-065A-421812 | Sequence 421812, |
| C 4 | 18.4 | 92.0 | 562 | 9 US-10-301-480-44854 | Sequence 44854, A |
| C 5 | 18.4 | 92.0 | 562 | 10 US-10-301-480-658263 | Sequence 658263, |
| C 6 | 18.4 | 92.0 | 740 | 6 US-09-925-065A-820255 | Sequence 820255, |
| C 7 | 18.4 | 92.0 | 186442 | 14 US-11-121-086-104 | Sequence 104, App |
| C 8 | 17.4 | 87.0 | 487 | 6 US-09-925-065A-174746 | Sequence 174746, |
| C 9 | 17.4 | 87.0 | 497 | 10 US-10-301-480-266137 | Sequence 266137, |
| C 10 | 17.4 | 87.0 | 497 | 10 US-10-301-480-879546 | Sequence 879546, |
| C 11 | 17.4 | 87.0 | 575 | 6 US-09-925-065A-115209 | Sequence 115209, |
| C 12 | 17.4 | 87.0 | 581 | 9 US-10-301-480-214195 | Sequence 214195, |
| C 13 | 17.4 | 87.0 | 581 | 10 US-10-301-480-827604 | Sequence 827604, |
| C 14 | 17.4 | 87.0 | 592 | 6 US-09-925-065A-159892 | Sequence 159892, |
| C 15 | 17.4 | 87.0 | 593 | 10 US-10-301-480-252732 | Sequence 252732, |
| C 16 | 17.4 | 87.0 | 593 | 10 US-10-301-480-866141 | Sequence 866141, |
| C 17 | 17.4 | 87.0 | 620 | 6 US-09-925-065A-880084 | Sequence 880084, |
| C 18 | 17.4 | 87.0 | 626 | 6 US-09-925-065A-298915 | Sequence 298915, |

ALIGNMENTS

| | | | | | |
|------|------|------|--------|--------------------------|-------------------|
| 19 | 17.4 | 87.0 | 627 | 10 US-10-301-480-375537 | Sequence 375537, |
| 20 | 17.4 | 87.0 | 627 | 10 US-10-301-480-988946 | Sequence 988946, |
| 21 | 17.4 | 87.0 | 998 | 10 US-10-301-480-595919 | Sequence 595919, |
| 22 | 17.4 | 87.0 | 998 | 10 US-10-301-480-1209328 | Sequence 1209328, |
| C 23 | 17.4 | 87.0 | 1203 | 9 US-10-301-480-29615 | Sequence 29615, A |
| C 24 | 17.4 | 87.0 | 1203 | 10 US-10-301-480-643024 | Sequence 643024, |
| C 25 | 17.4 | 87.0 | 2022 | 8 US-10-750-185-37655 | Sequence 37655, A |
| C 26 | 17.4 | 87.0 | 2022 | 8 US-10-750-623-37655 | Sequence 37655, A |
| C 27 | 17.4 | 87.0 | 3391 | 6 US-09-925-065A-711120 | Sequence 711120, |
| C 28 | 17.4 | 87.0 | 538 | 6 US-09-925-065A-246840 | Sequence 246840, |
| C 29 | 17.4 | 87.0 | 556 | 6 US-10-301-480-326998 | Sequence 326998, |
| C 30 | 17.4 | 87.0 | 556 | 10 US-10-301-480-940407 | Sequence 940407, |
| C 31 | 17.4 | 87.0 | 570 | 6 US-09-925-065A-787934 | Sequence 787934, |
| C 32 | 17.4 | 87.0 | 613 | 6 US-09-925-065A-190240 | Sequence 190240, |
| C 33 | 17.4 | 87.0 | 613 | 6 US-09-925-065A-190240 | Sequence 190240, |
| C 34 | 17.4 | 87.0 | 617 | 10 US-10-301-480-279974 | Sequence 279974, |
| C 35 | 17.4 | 87.0 | 617 | 10 US-10-301-480-279975 | Sequence 279975, |
| C 36 | 17.4 | 87.0 | 617 | 10 US-10-301-480-893383 | Sequence 893383, |
| C 37 | 17.4 | 87.0 | 617 | 10 US-10-301-480-893384 | Sequence 893384, |
| C 38 | 17.4 | 87.0 | 100000 | 14 US-11-124-367A-5091 | Sequence 5091, Ap |
| C 39 | 16.8 | 84.0 | 201 | 8 US-10-995-561-19356 | Sequence 19356, A |
| C 40 | 16.8 | 84.0 | 436 | 9 US-10-301-480-3003 | Sequence 3003, Ap |
| C 41 | 16.8 | 84.0 | 436 | 10 US-10-301-480-616412 | Sequence 616412, |
| C 42 | 16.8 | 84.0 | 443 | 6 US-09-925-065A-617358 | Sequence 617358, |
| C 43 | 16.8 | 84.0 | 477 | 6 US-09-925-065A-599889 | Sequence 599889, |
| C 44 | 16.8 | 84.0 | 491 | 6 US-09-925-065A-372151 | Sequence 372151, |
| C 45 | 16.8 | 84.0 | 502 | 9 US-10-301-480-3216 | Sequence 3216, Ap |

RESULT 1
US-10-301-480-486528/c
; Sequence 486528, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 486528
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-486528

Query Match 92.0%; Score 18.4; DB 10; Length 529;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATTTTAAAGCAACAAATTAA 20
Db 41 ATTTTAAAGCAACAAATTAA 22

RESULT 2
US-10-301-480-109937/c
; Sequence 109937, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 2.99496 Seconds
(Without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-6

Perfect score: 15
Sequence: 1 aattattctgtgtg 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/ina/1.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfillseq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 15 | 100.0 | 612 | US-09-248-796A-1530 | Sequence 1530, App |
| 2 | 15 | 100.0 | 903 | US-09-270-767-12919 | Sequence 12919, A |
| 3 | 15 | 100.0 | 2989 | US-08-956-171E-150 | Sequence 150, App |
| 4 | 15 | 100.0 | 2989 | US-08-781-986A-150 | Sequence 150, App |
| 5 | 15 | 100.0 | 317366 | US-09-949-016-16001 | Sequence 16001, A |
| 6 | 14 | 93.3 | 467 | US-09-280-11E-89 | Sequence 89, App1 |
| 7 | 14 | 93.3 | 601 | US-09-949-016-53768 | Sequence 53768, A |
| 8 | 14 | 93.3 | 601 | US-09-949-016-143167 | Sequence 143167, A |
| 9 | 14 | 93.3 | 601 | US-09-949-016-144554 | Sequence 144554, A |
| 10 | 14 | 93.3 | 601 | US-09-949-016-144555 | Sequence 144555, A |
| 11 | 14 | 93.3 | 686 | US-09-270-767-5402 | Sequence 5402, App |
| 12 | 14 | 93.3 | 686 | US-09-270-767-20684 | Sequence 20684, A |
| 13 | 14 | 93.3 | 2241 | PCR-US95-10509-1 | Sequence 1, App1 |
| 14 | 14 | 93.3 | 3517 | US-10-104-047-647 | Sequence 11, App1 |
| 15 | 14 | 93.3 | 3526 | US-09-976-594-11 | Sequence 15, App1 |
| 16 | 14 | 93.3 | 3680 | US-09-647-590-15 | Sequence 268, App |
| 17 | 14 | 93.3 | 6617 | US-09-976-594-268 | Sequence 14075, A |
| 18 | 14 | 93.3 | 12951 | US-09-949-016-14075 | Sequence 647, App |
| 19 | 14 | 93.3 | 14759 | US-09-661-887-1 | Sequence 14075, A |
| 20 | 14 | 93.3 | 15203 | US-09-949-016-16410 | Sequence 16410, A |
| 21 | 14 | 93.3 | 17580 | US-09-949-016-16055 | Sequence 16055, A |
| 22 | 14 | 93.3 | 36075 | US-09-949-016-16571 | Sequence 16571, A |
| 23 | 14 | 93.3 | 36075 | US-09-949-016-16572 | Sequence 16572, A |
| 24 | 14 | 93.3 | 36625 | US-09-949-016-12788 | Sequence 12788, A |

| | | | | | |
|----|----|------|-------|---------------------|-------------------|
| 25 | 14 | 93.3 | 37133 | US-09-949-016-16569 | Sequence 16569, A |
| 26 | 14 | 93.3 | 37133 | US-09-949-016-16570 | Sequence 16570, A |
| 27 | 14 | 93.3 | 44393 | US-09-949-016-14944 | Sequence 14944, A |
| 28 | 14 | 93.3 | 44393 | US-09-949-016-14945 | Sequence 14945, A |
| 29 | 14 | 93.3 | 44393 | US-09-949-016-14946 | Sequence 14946, A |
| 30 | 14 | 93.3 | 44393 | US-09-949-016-16811 | Sequence 16811, A |
| 31 | 14 | 93.3 | 50563 | US-09-949-016-15821 | Sequence 15821, A |
| 32 | 14 | 93.3 | 69709 | US-09-949-016-15784 | Sequence 15784, A |
| 33 | 14 | 93.3 | 72662 | US-09-949-016-17073 | Sequence 17073, A |
| 34 | 14 | 93.3 | 78846 | US-09-949-016-12396 | Sequence 12396, A |
| 35 | 14 | 93.3 | 78846 | US-09-949-016-12791 | Sequence 12791, A |
| 36 | 14 | 93.3 | 78846 | US-09-949-016-12792 | Sequence 12792, A |
| 37 | 14 | 93.3 | 78846 | US-09-949-016-12793 | Sequence 12793, A |
| 38 | 14 | 93.3 | 78850 | US-09-949-016-16013 | Sequence 16013, A |
| 39 | 14 | 93.3 | 78850 | US-09-949-016-16014 | Sequence 16014, A |
| 40 | 14 | 93.3 | 78850 | US-09-949-016-16015 | Sequence 16015, A |
| 41 | 14 | 93.3 | 78850 | US-09-949-016-16016 | Sequence 16016, A |
| 42 | 14 | 93.3 | 78850 | US-09-949-016-16201 | Sequence 16201, A |
| 43 | 14 | 93.3 | 78850 | US-09-949-016-16202 | Sequence 16202, A |
| 44 | 14 | 93.3 | 78850 | US-09-949-016-16203 | Sequence 16203, A |
| 45 | 14 | 93.3 | 78850 | US-09-949-016-16204 | Sequence 16204, A |

ALIGNMENTS

RESULT 1
US-09-248-796A-1530/C
; Sequence 1530, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1530
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1530

Query Match 100.0%; Score 15; DB 3; Length 612;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AATTATTGTTG 15
|||||
DB 20 AATTATTGTTG 6

RESULT 2
US-09-270-767-12919/C
; Sequence 12919, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 12919
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Drosophila melanogaster

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 85.8732 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aattatttgcgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: gb_esc2:*
3: gb_esc3:*
4: gb_hlc:*
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7: gb_esc6:*
8: gb_esc7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 15 | 100.0 | 137 | 3 | BI324061 |
| 3 | 15 | 100.0 | 161 | 10 | BM124334 |
| 4 | 15 | 100.0 | 163 | 1 | AM522511 |
| 5 | 15 | 100.0 | 183 | 10 | C2365564 |
| 6 | 15 | 100.0 | 183 | 10 | BM190591 |
| 7 | 15 | 100.0 | 185 | 9 | CC095316 |
| 8 | 15 | 100.0 | 216 | 9 | CC095316 |
| 9 | 15 | 100.0 | 217 | 9 | CC746949 |
| 10 | 15 | 100.0 | 234 | 1 | AV240038 |
| 11 | 15 | 100.0 | 248 | 10 | CG408145 |
| 12 | 15 | 100.0 | 252 | 10 | CL446525 |
| 13 | 15 | 100.0 | 254 | 9 | CC676891 |
| 14 | 15 | 100.0 | 278 | 10 | CG904523 |
| 15 | 15 | 100.0 | 280 | 2 | BM410707 |
| 16 | 15 | 100.0 | 284 | 10 | CG091593 |
| 17 | 15 | 100.0 | 286 | 10 | CL226055 |
| 18 | 15 | 100.0 | 289 | 10 | CG091695 |
| 19 | 15 | 100.0 | 295 | 9 | CE238834 |
| 20 | 15 | 100.0 | 313 | 8 | T01835 |
| 21 | 15 | 100.0 | 313 | 10 | CG720870 |
| 22 | 15 | 100.0 | 322 | 10 | CL449105 |

| | | | | | | |
|------|----|-------|-----|----|----------|--------------------|
| C 23 | 15 | 100.0 | 324 | 9 | CC787357 | CC787357 ZMABB015 |
| C 24 | 15 | 100.0 | 327 | 10 | CG873320 | CG873320 ZMABB028 |
| C 25 | 15 | 100.0 | 333 | 1 | AM165275 | AM165275 f606b07.x |
| C 26 | 15 | 100.0 | 338 | 2 | BG301524 | BG301524 KC02D09.y |
| C 27 | 15 | 100.0 | 341 | 2 | BG301665 | BG301665 KC03h12.y |
| C 28 | 15 | 100.0 | 341 | 7 | CV475153 | CV475153 23648.1.D |
| C 29 | 15 | 100.0 | 344 | 10 | BM157285 | BM157285 Danto rer |
| C 30 | 15 | 100.0 | 346 | 9 | CC761571 | CC761571 ZMABB021 |
| C 31 | 15 | 100.0 | 347 | 2 | BG301417 | BG301417 KC04B02.y |
| C 32 | 15 | 100.0 | 348 | 5 | BY577034 | BY577034 BY577034 |
| C 33 | 15 | 100.0 | 351 | 9 | CC382054 | CC382054 PUKKD05TB |
| C 34 | 15 | 100.0 | 352 | 2 | BG301541 | BG301541 KC02d03.y |
| C 35 | 15 | 100.0 | 356 | 10 | CG422080 | CG422080 ZMABB003 |
| C 36 | 15 | 100.0 | 357 | 2 | BG301903 | BG301903 KC07d01.y |
| C 37 | 15 | 100.0 | 357 | 10 | CG876818 | CG876818 ZMABB028 |
| C 38 | 15 | 100.0 | 362 | 5 | BQ479395 | BQ479395 ku35b03.y |
| C 39 | 15 | 100.0 | 367 | 10 | CG994153 | CG994153 ZMABB0037 |
| C 40 | 15 | 100.0 | 376 | 10 | CG315201 | CG315201 ZMABB038 |
| C 41 | 15 | 100.0 | 381 | 2 | BG301858 | BG301858 KC06C09.y |
| C 42 | 15 | 100.0 | 384 | 10 | CL395037 | CL395037 ZMABB021 |
| C 43 | 15 | 100.0 | 385 | 9 | AQ023189 | AQ023189 HS_2177_B |
| C 44 | 15 | 100.0 | 396 | 2 | BG301349 | BG301349 KC04c11.y |
| C 45 | 15 | 100.0 | 397 | 7 | CR419357 | CR419357 CR419357 |

ALIGNMENTS

RESULT 1
LOCUS CN872089 86 bp mRNA linear EST 04-JUN-2004
DEFINITION 010211AAPA002796HT (AAPA) Royal Gala 24 DAFB fruit Malus x domestic
domestic cDNA clone AAPA002796, mRNA sequence.

VERSION CN872089
KEYWORDS CN872089.1 GI:48258247
SOURCE EST.
ORGANISM Malus x domestica
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside 1; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 86)
AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Jansen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
TITLE HortResearch Apple Est Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES

source location/Qualifiers
1..86
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAPA002796"
/tissue_type="Fruit"
/dev_stage="24 days after full bloom"
/clone_lib="(AAPA) Royal Gala 24 DAFB fruit"
/note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"

ORIGIN

Query Match 100.0%; Score 15; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATTATTGTTGTTG 15
|||||
Db 53 AATTATTGTTGTTG 67

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 12.2768 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aattctctgtctgtc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseq20008:*
4: geneseq20018:*
5: geneseq20028:*
6: geneseq20038:*
7: geneseq20048:*
8: geneseq20058:*
9: geneseq20068:*
10: geneseq20078:*
11: geneseq20088:*
12: geneseq20098:*
13: geneseq20108:*
14: geneseq20118:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 15 | 100.0 | 15 | 13 | ADT08247 |
| 2 | 15 | 100.0 | 15 | 13 | ADT89055 |
| 3 | 15 | 100.0 | 201 | 13 | ADT89055 |
| 4 | 15 | 100.0 | 315 | 8 | ACF75120 |
| 5 | 15 | 100.0 | 435 | 13 | ADT08242 |
| 6 | 15 | 100.0 | 435 | 13 | ADT89050 |
| 7 | 15 | 100.0 | 480 | 13 | ADT08271 |
| 8 | 15 | 100.0 | 480 | 13 | ADT89079 |
| 9 | 15 | 100.0 | 501 | 3 | AAA45092 |
| 10 | 15 | 100.0 | 554 | 6 | ABQ27596 |
| 11 | 15 | 100.0 | 554 | 6 | ABQ27597 |
| 12 | 15 | 100.0 | 555 | 6 | ABQ33730 |
| 13 | 15 | 100.0 | 555 | 6 | ABQ33731 |
| 14 | 15 | 100.0 | 733 | 13 | ADT89052 |
| 15 | 15 | 100.0 | 2033 | 13 | ADT08244 |
| 16 | 15 | 100.0 | 2033 | 13 | ADT89052 |
| 17 | 15 | 100.0 | 2783 | 13 | ADT08243 |
| 18 | 15 | 100.0 | 2783 | 13 | ADT89051 |
| 19 | 15 | 100.0 | 2960 | 13 | ADT89080 |

| | | | | | | | | |
|---|----|----|-------|--------|----|----------|----------|---------------------|
| C | 20 | 15 | 100.0 | 2989 | 2 | AAV74461 | AAV74461 | Staphyloc |
| | 21 | 15 | 100.0 | 4110 | 4 | ABL07042 | ABL07042 | Drosophila |
| | 22 | 15 | 100.0 | 4986 | 4 | ABL05843 | ABL05843 | Human rep |
| | 23 | 15 | 100.0 | 4986 | 4 | ABL98407 | ABL98407 | Human tes |
| | 24 | 15 | 100.0 | 5146 | 10 | ADD48890 | ADD48890 | Human gen |
| | 25 | 15 | 100.0 | 5542 | 6 | ABL34021 | ABL34021 | Human imm |
| | 26 | 15 | 100.0 | 6197 | 6 | ABL33711 | ABL33711 | Human imm |
| | 27 | 15 | 100.0 | 6436 | 6 | ABL32681 | ABL32681 | Human imm |
| | 28 | 15 | 100.0 | 11806 | 8 | ACA22763 | ACA22763 | Prokaryot |
| | 29 | 15 | 100.0 | 14598 | 4 | AAK80680 | AAK80680 | Human imm |
| | 30 | 15 | 100.0 | 14598 | 4 | AAK79627 | AAK79627 | Human imm |
| | 31 | 15 | 100.0 | 110000 | 6 | ABQ67196 | ABQ67196 | Continuation (6 of |
| | 32 | 15 | 100.0 | 110000 | 6 | ABQ69245 | ABQ69245 | Continuation (28 of |
| | 33 | 15 | 100.0 | 110000 | 8 | ABX16390 | ABX16390 | Mouse hlg |
| | 34 | 15 | 100.0 | 110000 | 12 | ADO34435 | ADO34435 | Continuation (6 of |
| | 35 | 15 | 100.0 | 154799 | 13 | ADS36467 | ADS36467 | Continuation (6 of |
| | 36 | 15 | 100.0 | 235962 | 14 | ADZ12926 | ADZ12926 | Human aut |
| | 37 | 14 | 93.3 | 41 | 6 | AB249694 | AB249694 | Murine ca |
| | 38 | 14 | 93.3 | 41 | 6 | AB243541 | AB243541 | Human bul |
| | 39 | 14 | 93.3 | 49 | 8 | ACC00253 | ACC00253 | rapl gene |
| | 40 | 14 | 93.3 | 50 | 8 | ACC00242 | ACC00242 | rapl gene |
| | 41 | 14 | 93.3 | 141 | 12 | ADG99575 | ADG99575 | Kidney di |
| | 42 | 14 | 93.3 | 266 | 2 | AAQ77295 | AAQ77295 | Human gen |
| | 43 | 14 | 93.3 | 380 | 6 | ABL64512 | ABL64512 | Stomach c |
| | 44 | 14 | 93.3 | 380 | 6 | ABL67566 | ABL67566 | Oesophagu |
| | 45 | 14 | 93.3 | 395 | 4 | AAI00951 | AAI00951 | Human rep |

ALIGNMENTS

| | | | |
|----------|---|---|-----------------------|
| RESULT 1 | ADT08247 | ADT08247 | standard; DNA; 15 BP. |
| ID | ADT08247 | ADT08247 | (first entry) |
| AC | ADT08247 | ADT08247 | |
| XX | 13-JUN-2005 | 13-JUN-2005 | |
| DE | Zebrafish L-FABP upstream region HNF-1alpha binding site. | Zebrafish L-FABP upstream region HNF-1alpha binding site. | |
| XX | Zebrafish; ds; liver fatty acid binding protein; L-FABP; | Zebrafish; ds; liver fatty acid binding protein; L-FABP; | |
| KM | liver regulatory element; LR; transgenic; HNF(1); HNF(2); HNF-1alpha; | liver regulatory element; LR; transgenic; HNF(1); HNF(2); HNF-1alpha; | |
| KM | HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP; | HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP; | |
| KM | liver development; liver disease; liver necrosis; liver cancer. | liver development; liver disease; liver necrosis; liver cancer. | |
| OS | Danio rerio. | Danio rerio. | |
| XX | US2004209833-A1. | US2004209833-A1. | |
| PN | 21-OCT-2004. | 21-OCT-2004. | |
| XX | 21-NOV-2003; 2003US-00717573. | 21-NOV-2003; 2003US-00717573. | |
| PF | 16-APR-2003; 2003US-0463035P. | 16-APR-2003; 2003US-0463035P. | |
| PR | 27-MAY-2003; 2003US-0473210P. | 27-MAY-2003; 2003US-0473210P. | |
| XX | (WUJ/) WU J. | (WUJ/) WU J. | |
| PA | (HERG/) HER G M. | (HERG/) HER G M. | |
| PI | Wu J, Her GM; | Wu J, Her GM; | |
| XX | WPI; 2004-765481/75. | WPI; 2004-765481/75. | |
| DR | New isolated polynucleotide useful for generating transgenic fish such as | New isolated polynucleotide useful for generating transgenic fish such as | |
| XX | pt zebrafish, comprises liver-specific expression control sequence that | pt zebrafish, comprises liver-specific expression control sequence that | |
| PT | modulates expression of vertebrate liver fatty acid binding protein. | modulates expression of vertebrate liver fatty acid binding protein. | |
| XX | Claim 4; SEQ ID NO 6; 40bp; English. | Claim 4; SEQ ID NO 6; 40bp; English. | |
| PS | The invention relates to an isolated polynucleotide comprising a liver- | The invention relates to an isolated polynucleotide comprising a liver- | |
| XX | specific expression control sequence (LR) which modulates expression of a | specific expression control sequence (LR) which modulates expression of a | |
| CC | vertebrate liver fatty acid binding protein (L-FABP). Also included are a | vertebrate liver fatty acid binding protein (L-FABP). Also included are a | |

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OM nucleic - nucleic search, using bw model

Run on: April 1, 2006, 05:44:25 ; Search time 89.238 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-6

Perfect score: 15
Sequence: 1 aatttattgtgtg 15

Scoring table: IDENTITY_NUC

Searched: 5883141 begs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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|------------------|---------------|--------------|
| Post-processing: | Minimum Match | 0% |
| | Maximum Match | 100% |
| | Listing first | 45 summaries |

Database :

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2:  gb_ba.*
3:  gb_in.*
4:  gb_env.*
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6:  gb_ov.*
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9:  gb_pr.*
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15: gb_hcr.*
    gb_pl.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|------|--------------------|----------------------------|
| c | 1 | 15 | 100.0 | 201 | 6 | CQ930101 Sequence |
| c | 2 | 15 | 100.0 | 314 | 10 | AU026431 Rattus no |
| c | 3 | 15 | 100.0 | 315 | 6 | AX622636 Sequence |
| 4 | 15 | 100.0 | 486 | 10 | BV165522 PDKXN1-1 | |
| 5 | 15 | 100.0 | 486 | 10 | BV165522 PDKXN1-2 | |
| 6 | 15 | 100.0 | 500 | 2 | X89080 C.elegans d | |
| c | 7 | 15 | 100.0 | 570 | 13 | AY136052 HIV-1 1st |
| c | 8 | 15 | 100.0 | 570 | 13 | AY136070 HIV-1 1st |
| c | 9 | 15 | 100.0 | 592 | 10 | BV677735 ST18_2399 |
| c | 10 | 15 | 100.0 | 612 | 6 | AR546399 Sequence |
| c | 11 | 15 | 100.0 | 630 | 10 | BV257210 S23P522 |
| c | 12 | 15 | 100.0 | 669 | 8 | HSA332937 Homo sapi |
| c | 13 | 15 | 100.0 | 698 | 10 | BV594471 B35964471 |
| c | 14 | 15 | 100.0 | 756 | 10 | BV618937 S215P6833 |
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| 28 | 15 | 100.0 | 6197 | 6 | AX346613 |
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| 31 | 15 | 100.0 | 6436 | 6 | AX345583 |
| 32 | 15 | 100.0 | 7515 | 5 | BX908746 |
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| 34 | 15 | 100.0 | 11784 | 2 | AY317337 |
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| 37 | 15 | 100.0 | 19722 | 5 | AL935210 |
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| | | | | | AF512598 Dario rer |
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| | | | | | CR936480 Zebrafish |
| | | | | | AL959067 Haemochu |
| | | | | | AL935210 Zebrafish |
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| | | | | | AP000291 Homo sapi |
| | | | | | AC020390 Drosophila |
| | | | | | CR936413 Zebrafish |
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ALIGNMENTS

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VERSION     CG930101.1   GI:56219491
KEYWORDS
SOURCE
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            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS   Cargill,M., Begovich,A.B. and Alexander,H.C.
TITLE     Genetic polymorphisms associated with rheumatoid arthritis, methods
of detection and uses thereof
JOURNAL   Patent: WO 2004083403-A 5134 30-SEP-2004;
Applera Corporation (US)
FEATURES   Location/Qualifiers
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Db        198 AATTATTTGTGTTG 184

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LOCUS      AU026431/c          314 bp      DNA           linear    STS 02-MAR-1999
DEFINITION Ratius norvegicus, OTSUKA clone, OTS4.09/954c07, microsatellite
ACCESSION  AU026431
VERSION     AU026431.1   GI:4516354
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match              100.0%; Score 15; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy       1 AATTATTTGTGTTG 15
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Db        198 AATTATTTGTGTTG 184

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-10-717-573-6

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Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| C 16 | 15 | 100.0 | 526 | 10 | US-10-301-480-1013117 |
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| C 20 | 15 | 100.0 | 540 | 6 | US-09-925-065A-342956 | Sequence 342956, |
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| C 23 | 15 | 100.0 | 553 | 9 | US-10-301-480-4386 | Sequence 4386, Ap |
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| C 25 | 15 | 100.0 | 563 | 6 | US-09-925-065A-164580 | Sequence 164580, |
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| C 31 | 15 | 100.0 | 604 | 6 | US-09-925-065A-581603 | Sequence 581603, |
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| C 33 | 15 | 100.0 | 615 | 6 | US-09-925-065A-531920 | Sequence 531920, |
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| C 39 | 15 | 100.0 | 675 | 6 | US-09-925-065A-899678 | Sequence 899678, |
| C 40 | 15 | 100.0 | 694 | 6 | US-09-925-065A-548225 | Sequence 548225, |
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US-11-128-061-5461/c
Sequence 5461, Application US/1128061
Publication No. US2006003958A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OR INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128, 061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5461
LENGTH: 248
TYPE: DNA
ORGANISM: *Cricetulus griseus*
US-11-128-061-5461
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Best Local Similarity 100.0%; Pred. No. 8.4e+02;
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RESULT 2
US-11-128-049-5461/c
Sequence 5461, Application US/1128049
Publication No. US20060010513A1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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| c 42 | 15 | 100.0 | 675 4 | US-09-925-065A-548225 | Sequence 548225, A |
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Sequence 6, Application US/10677254
Publication No. US20040209279A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
APPLICANT: HER, Guor Mour
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
FILE REFERENCE: 33151-188802
CURRENT FILING DATE: 2003-10-03
CURRENT OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 15
TYPE: DNA
ORGANISM: Danio rerio
US-10-677-254-6

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Sequence 6, Application US/10717573
Publication No. US20040209833A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
APPLICANT: HER, Guor Mour
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
FILE REFERENCE: 33151-188802
CURRENT FILING DATE: 2003-11-21
CURRENT APPLICATION NUMBER: US/10/717,573
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 15
TYPE: DNA

GenCore version 5.1.7
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| 19 | 13 | 100.0 | 601 | US-09-949-016-129026 | Sequence 129026, A |
| 20 | 13 | 100.0 | 601 | US-09-949-016-142486 | Sequence 142486, A |
| 21 | 13 | 100.0 | 601 | US-09-949-016-178033 | Sequence 178033, A |
| 22 | 13 | 100.0 | 601 | US-09-949-016-178034 | Sequence 178034, A |
| 23 | 13 | 100.0 | 601 | US-09-949-016-189483 | Sequence 189483, A |
| 24 | 13 | 100.0 | 601 | US-09-949-016-201247 | Sequence 201247, A |

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| c 25 | 13 | 100.0 | 601 | 3 | US-09-949-016-201361 | Sequence 201361, A |
| c 26 | 13 | 100.0 | 736 | 3 | US-09-270-767-10249 | Sequence 10249, A |
| c 27 | 13 | 100.0 | 825 | 3 | US-09-270-767-12216 | Sequence 12216, A |
| c 28 | 13 | 100.0 | 965 | 3 | US-09-270-767-9078 | Sequence 9078, AP |
| c 29 | 13 | 100.0 | 965 | 3 | US-09-270-767-24360 | Sequence 24360, A |
| c 30 | 13 | 100.0 | 1693 | 3 | US-09-149-476-224 | Sequence 224, AP |
| c 31 | 13 | 100.0 | 1753 | 3 | US-09-149-476-56 | Sequence 56, AP |
| c 32 | 13 | 100.0 | 1753 | 3 | US-08-750-717-1 | Sequence 1, Appl |
| c 33 | 13 | 100.0 | 15379 | 3 | US-09-949-016-14191 | Sequence 14191, A |
| c 34 | 13 | 100.0 | 20634 | 3 | US-09-949-016-16627 | Sequence 16627, A |
| c 35 | 13 | 100.0 | 32868 | 3 | US-09-949-016-17406 | Sequence 17406, A |
| c 36 | 13 | 100.0 | 32519 | 3 | US-09-949-016-17165 | Sequence 17165, A |
| c 37 | 13 | 100.0 | 37385 | 3 | US-09-949-016-12466 | Sequence 12466, A |
| c 38 | 13 | 100.0 | 37388 | 3 | US-09-949-016-16846 | Sequence 16846, A |
| c 39 | 13 | 100.0 | 56551 | 3 | US-09-949-016-12030 | Sequence 12030, A |
| c 40 | 13 | 100.0 | 83851 | 3 | US-09-949-016-13847 | Sequence 13847, A |
| c 41 | 13 | 100.0 | 86956 | 3 | US-09-949-016-12994 | Sequence 12994, A |
| c 42 | 13 | 100.0 | 105050 | 3 | US-09-949-016-15953 | Sequence 15953, A |
| c 43 | 13 | 100.0 | 118999 | 3 | US-09-791-105B-32 | Sequence 32, Appl |
| c 44 | 13 | 100.0 | 118999 | 3 | US-09-791-105B-32 | Sequence 32, Appl |
| c 45 | 13 | 100.0 | 134890 | 3 | US-09-949-016-15602 | Sequence 15602, A |

ALIGNMENTS

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RESULT 1
US-09-248-796A-8945/C
; Sequence 8945, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8945
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-8945

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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      186 AAATAAACAGGG 174

RESULT 2
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; Sequence 1864, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; CURRENT APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1864

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 74.4234 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 13 | 100.0 | 94 | 7 CN868582 | CN868582 001116AAO |
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| 5 | 13 | 100.0 | 105 | 1 AQ925602 | AQ925602 RPCI-23-2 |
| 6 | 13 | 100.0 | 131 | 1 AI705517 | AI705517 UI-R-AC1- |
| 7 | 13 | 100.0 | 131 | 9 AQ372908 | AQ372908 RPCI11-15 |
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| 9 | 13 | 100.0 | 139 | 3 BJ252096 | BJ252096 |
| 10 | 13 | 100.0 | 143 | 9 AA247880 | AA247880 1M0245D17 |
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| 14 | 13 | 100.0 | 155 | 10 CG786368 | CG786368 ZMMBD011 |
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| 16 | 13 | 100.0 | 160 | 10 AG023082 | AG023082 Oryza sat |
| 17 | 13 | 100.0 | 161 | 3 BI631314 | BI631314 RH60867.5 |
| 18 | 13 | 100.0 | 162 | 9 BH116400 | BH116400 RPCI-24-3 |
| 19 | 13 | 100.0 | 163 | 9 BH327180 | BH327180 CH230-116 |
| 20 | 13 | 100.0 | 166 | 1 AL387438 | AL387438 MCB042E10 |
| 21 | 13 | 100.0 | 168 | 2 BI075074 | BI075074 IPL 20 DO |
| 22 | 13 | 100.0 | 168 | 9 AZ893740 | AZ893740 RPCI-24-1 |

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| 26 | 13 | 100.0 | 177 | 5 B0905285 | B0905285 Ta04 13e1 |
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| 29 | 13 | 100.0 | 187 | 6 CD938893 | CD938893 OV_111G05 |
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| 31 | 13 | 100.0 | 189 | 7 CK107033 | CK107033 CK107033 |
| 32 | 13 | 100.0 | 191 | 7 CO541293 | CO541293 Mdfrc3039 |
| 33 | 13 | 100.0 | 192 | 2 BF360687 | BF360687 QV4-OT003 |
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| 35 | 13 | 100.0 | 192 | 11 DR30F18T | DR30F18T |
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| 42 | 13 | 100.0 | 201 | 6 AV114315 | AV114315 AV114315 |
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ALIGNMENTS

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LOCUS BX153895 56 bp DNA linear GSS 28-JAN-2003
DEFINITION Danilo rerio genomic clone DKEX-116L22, genomic survey sequence.
ACCESSION BX153895
VERSION BX153895.1 GI:27985456

KEYWORDS GSS:
SOURCE Danilo rerio (zebrafish)
ORGANISM Danilo rerio
REFERENCE Humphray, S.J., Huckle, E. and Durham, J.L.
AUTHORS

TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Ganger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphrey@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 116L22. 116L22 is part of the Danilokey BAC library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/. Location/Qualifiers

FEATURES

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ORIGIN

Query Match 100.0%; Score 13; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATAAACGGG 13
|||||
Db 28 AAATAAACGGG 40

RESULT 2
LOCUS CF554321 92 bp mRNA linear EST 23-SEP-2003
DEFINITION SSHGw69 Subtracted library from infected wheat roots with

GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model

Run on: April 1, 2006, 05:16:37 ; Search time 10.6399 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-5
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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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14: geneeqn20118:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 13 | 100.0 | 13 | ADT89054 | Adt89054 Zebrafish |
| 3 | 13 | 100.0 | 217 | AAK62657 | AAK62657 Human lmm |
| 4 | 13 | 100.0 | 222 | ADH32082 | Adh32082 Yeast sma |
| 5 | 13 | 100.0 | 227 | AAK83013 | AAK83013 Human lmm |
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| 7 | 13 | 100.0 | 345 | ADD32698 | Add32698 Human mlt |
| 8 | 13 | 100.0 | 345 | AAK83015 | AAK83015 Human lmm |
| 9 | 13 | 100.0 | 349 | AAK83014 | AAK83014 Human lmm |
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| 13 | 13 | 100.0 | 435 | ADT89050 | Adt89050 Zebrafish |
| 14 | 13 | 100.0 | 439 | ACN58770 | ACN58770 Cotton gy |
| 15 | 13 | 100.0 | 458 | ADL88319 | Adl88319 DNA up-re |
| 16 | 13 | 100.0 | 458 | ADL88320 | Adl88320 DNA up-re |
| 17 | 13 | 100.0 | 480 | ADT08271 | Adt08271 Zebrafish |
| 18 | 13 | 100.0 | 480 | ADT89079 | Adt89079 Zebrafish |
| 19 | 13 | 100.0 | 493 | ABV51847 | Abv51847 Human pro |

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| 22 | 13 | 100.0 | 508 | 15 | ABA14249 | ABA14249 Human net |
| 23 | 13 | 100.0 | 512 | 12 | ADP66310 | ADP66310 Human CDN |
| 24 | 13 | 100.0 | 522 | 4 | ABA89508 | ABA89508 Escherich |
| 25 | 13 | 100.0 | 563 | 5 | AD168794 | Ad168794 Human ova |
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| 27 | 13 | 100.0 | 566 | 5 | ABV50018 | Abv50018 Human pro |
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| 29 | 13 | 100.0 | 603 | 13 | ACN50391 | ACN50391 Cotton no |
| 30 | 13 | 100.0 | 649 | 13 | ADP61743 | ADP61743 Cotton CD |
| 31 | 13 | 100.0 | 668 | 6 | ABE89601 | ABE89601 Human pol |
| 32 | 13 | 100.0 | 720 | 13 | ADT48592 | ADT48592 Bacterial |
| 33 | 13 | 100.0 | 759 | 4 | AA194754 | AA194754 Human neu |
| 34 | 13 | 100.0 | 807 | 4 | AA242245 | AA242245 Human nor |
| 35 | 13 | 100.0 | 818 | 8 | ABV77452 | Abv77452 P. monodo |
| 36 | 13 | 100.0 | 820 | 13 | ADP18958 | ADP18958 Plant CDN |
| 37 | 13 | 100.0 | 830 | 5 | AA63164 | AA63164 Human pur |
| 38 | 13 | 100.0 | 987 | 13 | ADT45337 | ADT45337 Bacterial |
| 39 | 13 | 100.0 | 1011 | 10 | ACP68641 | ACP68641 Phototrab |
| 40 | 13 | 100.0 | 1113 | 5 | ADM19419 | ADM19419 Novel hum |
| 41 | 13 | 100.0 | 1206 | 5 | AAH94515 | AAH94515 Human foe |
| 42 | 13 | 100.0 | 1312 | 13 | ADR60819 | ADR60819 Cotton CD |
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ALIGNMENTS

RESULT 1
ADT08246
ID ADT08246 standard; DNA, 13 BP.

AC ADT08246;
XX
DT 13-JAN-2005 (first entry)

XX Zebrafish L-PABP upstream region HFH(2) binding site.

XX Zebrafish; ds; liver fatty acid binding protein; L-PABP;
XX liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
XX HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
XX liver development; liver disease; liver necrosis; liver cancer.

OS Danio rerio.

XX US2004209833-A1.

XX 21-OCT-2004.

XX 21-NOV-2003; 2003US-00717573.

XX 16-APR-2003; 2003US-0463035P.
XX 27-MAY-2003; 2003US-0473210P.

XX (WUJ/) WU J.
XX (HERG/) HER G M.

XX WU J, Her GM,
XX WPI, 2004-765481/75.

XX New isolated polynucleotide useful for generating transgenic fish such as
XX zebrafish, comprises liver-specific expression control sequence that
XX modulates expression of vertebrate liver fatty acid binding protein.

XX Claim 4; SEQ ID NO 5, 40pp; English.

XX The invention relates to an isolated polynucleotide comprising a liver-
XX specific expression control sequence (LR) which modulates expression of a
XX vertebrate liver fatty acid binding protein (L-PABP). Also included are a

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 77.3396 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 13 | 100.0 | 263 | 10 | BV288965 S232P689F |
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| 8 | 13 | 100.0 | 325 | 15 | SC298154 Z98153 Secale cere |
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| 10 | 13 | 100.0 | 333 | 10 | GI0386 CQ431150 human STS C |
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| 39 | 13 | 100.0 | 470 | 3 | AY350324 AY350324 Unculture |
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ALIGNMENTS

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DEFINITION Sequence 4824 from Patent WO02070737.
ACCESSION CO659898
VERSION CO659898.1 GI:42129537

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Liaw,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 4824 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 52 AAATTAACAGGG 64
64 |||||||||

RESULT 2
LOCUS AR553814/c 204 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 8945 from patent US 6747137.
ACCESSION AR553814
VERSION AR553814.1 GI:53946989
KEYWORDS
SOURCE Unknown.

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Title: US-10-717-573-5
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Sequence: 1 aaaaataacaggg 13

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Gapop 10.0, Gapext 1.0

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 13 | 100.0 | 25 | 8 | US-10-310-914A-70682 |
| 2 | 13 | 100.0 | 201 | 8 | US-10-995-561-45580 |
| 3 | 13 | 100.0 | 201 | 8 | US-10-995-561-45604 |
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| 5 | 13 | 100.0 | 201 | 8 | US-10-995-561-45620 |
| 6 | 13 | 100.0 | 201 | 14 | US-11-124-368A-7480 |
| 7 | 13 | 100.0 | 201 | 14 | US-11-124-368A-7480 |
| 8 | 13 | 100.0 | 395 | 6 | US-09-925-065A-18255 |
| 9 | 13 | 100.0 | 397 | 10 | US-10-301-480-298130 |
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| 11 | 13 | 100.0 | 397 | 10 | US-10-301-480-911539 |
| 12 | 13 | 100.0 | 397 | 10 | US-10-301-480-911540 |
| 13 | 13 | 100.0 | 413 | 6 | US-09-925-065A-210863 |
| 14 | 13 | 100.0 | 413 | 6 | US-09-925-065A-210864 |
| 15 | 13 | 100.0 | 417 | 6 | US-09-925-065A-185779 |
| 16 | 13 | 100.0 | 428 | 10 | US-10-301-480-275560 |
| 17 | 13 | 100.0 | 428 | 10 | US-10-301-480-889569 |
| 18 | 13 | 100.0 | 437 | 6 | US-09-925-065A-856288 |

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| 19 | 13 | 100.0 | 447 | 6 | US-09-925-065A-952784 | Sequence 952784, |
| 20 | 13 | 100.0 | 459 | 9 | US-10-301-480-58009 | Sequence 58009, A |
| 21 | 13 | 100.0 | 459 | 9 | US-10-301-480-58010 | Sequence 58010, A |
| 22 | 13 | 100.0 | 459 | 10 | US-10-301-480-671418 | Sequence 671418, A |
| 23 | 13 | 100.0 | 459 | 10 | US-10-301-480-671419 | Sequence 671419, A |
| 24 | 13 | 100.0 | 461 | 10 | US-10-301-480-394300 | Sequence 394300, A |
| 25 | 13 | 100.0 | 461 | 10 | US-10-301-480-394301 | Sequence 394301, A |
| 26 | 13 | 100.0 | 461 | 10 | US-10-301-480-1007709 | Sequence 1007709, A |
| 27 | 13 | 100.0 | 461 | 10 | US-10-301-480-1007710 | Sequence 1007710, A |
| 28 | 13 | 100.0 | 466 | 6 | US-09-925-065A-873597 | Sequence 873597, A |
| 29 | 13 | 100.0 | 467 | 6 | US-09-925-065A-319550 | Sequence 319550, A |
| 30 | 13 | 100.0 | 467 | 6 | US-09-925-065A-319551 | Sequence 319551, A |
| 31 | 13 | 100.0 | 480 | 10 | US-10-301-480-554056 | Sequence 554056, A |
| 32 | 13 | 100.0 | 487 | 6 | US-10-301-480-1167465 | Sequence 1167465, A |
| 33 | 13 | 100.0 | 497 | 6 | US-09-925-065A-859863 | Sequence 859863, A |
| 34 | 13 | 100.0 | 497 | 6 | US-09-925-065A-859864 | Sequence 859864, A |
| 35 | 13 | 100.0 | 510 | 10 | US-10-301-480-479160 | Sequence 479160, A |
| 36 | 13 | 100.0 | 510 | 10 | US-10-301-480-1092569 | Sequence 1092569, A |
| 37 | 13 | 100.0 | 511 | 6 | US-09-925-065A-413114 | Sequence 413114, A |
| 38 | 13 | 100.0 | 514 | 6 | US-09-925-065A-315530 | Sequence 315530, A |
| 39 | 13 | 100.0 | 514 | 6 | US-09-925-065A-775950 | Sequence 775950, A |
| 40 | 13 | 100.0 | 514 | 10 | US-10-301-480-390539 | Sequence 390539, A |
| 41 | 13 | 100.0 | 514 | 10 | US-10-301-480-1003948 | Sequence 1003948, A |
| 42 | 13 | 100.0 | 529 | 6 | US-09-925-065A-501017 | Sequence 501017, A |
| 43 | 13 | 100.0 | 531 | 6 | US-09-925-065A-48752 | Sequence 48752, A |
| 44 | 13 | 100.0 | 531 | 9 | US-10-301-480-149990 | Sequence 149990, A |
| 45 | 13 | 100.0 | 531 | 10 | US-10-301-480-763399 | Sequence 763399, A |

ALIGNMENTS

RESULT 1
US-10-310-914A-70682
Sequence 70682, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200, CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 70682
LENGTH: 25
TYPE: RNA
ORGANISM: Human
US-10-310-914A-70682

Query Match 100.0%; Score 13; DB 8; Length 25;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAACAAGG 13
DB 10 AAAAAAACAAGG 22

RESULT 2
US-10-995-561-45580/c
Sequence 45580, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: C0001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 15.1561 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaataaacaggg 13

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 13 | 100.0 | 13 | US-10-677-254-5 | Sequence 5, Appl1 |
| 2 | 13 | 100.0 | 13 | US-10-717-573-5 | Sequence 5, Appl1 |
| 3 | 13 | 100.0 | 25 | US-10-719-956-112219 | Sequence 112219, |
| 4 | 13 | 100.0 | 25 | US-10-719-900-439757 | Sequence 439757, |
| 5 | 13 | 100.0 | 164 | US-10-242-535A-4824 | Sequence 4824, Ap |
| 6 | 13 | 100.0 | 164 | US-10-085-783A-4824 | Sequence 4824, Ap |
| 7 | 13 | 100.0 | 201 | US-10-741-601-23769 | Sequence 23769, A |
| 8 | 13 | 100.0 | 201 | US-10-719-993-13530 | Sequence 13530, A |
| 9 | 13 | 100.0 | 201 | US-10-741-600-57049 | Sequence 57049, A |
| 10 | 13 | 100.0 | 201 | US-10-741-600-59352 | Sequence 59352, A |
| 11 | 13 | 100.0 | 201 | US-10-741-600-59360 | Sequence 59360, A |
| 12 | 13 | 100.0 | 201 | US-10-741-600-59362 | Sequence 59362, A |
| 13 | 13 | 100.0 | 201 | US-10-741-600-54465 | Sequence 54465, A |
| 14 | 13 | 100.0 | 222 | US-10-083-357-540 | Sequence 540, App |
| 15 | 13 | 100.0 | 257 | US-10-027-632-6566 | Sequence 6566, Ap |
| 16 | 13 | 100.0 | 257 | US-10-027-632-6566 | Sequence 6566, Ap |
| 17 | 13 | 100.0 | 258 | US-10-424-599-131220 | Sequence 131220, A |
| 18 | 13 | 100.0 | 263 | US-10-424-599-28916 | Sequence 28916, A |
| 19 | 13 | 100.0 | 271 | US-10-425-115-6130 | Sequence 6130, Ap |
| 20 | 13 | 100.0 | 273 | US-10-674-124A-82 | Sequence 82, Appl |
| 21 | 13 | 100.0 | 283 | US-10-425-115-64382 | Sequence 64382, A |
| 22 | 13 | 100.0 | 335 | US-10-425-115-105793 | Sequence 105793, |
| 23 | 13 | 100.0 | 354 | US-10-424-599-126370 | Sequence 126370, |

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| c 24 | 13 | 100.0 | 354 | 8 | US-10-425-115-180952 | Sequence 180952, |
| c 25 | 13 | 100.0 | 361 | 7 | US-10-437-963-32988 | Sequence 32988, A |
| c 26 | 13 | 100.0 | 364 | 8 | US-10-425-115-17424 | Sequence 17424, A |
| c 27 | 13 | 100.0 | 366 | 7 | US-10-424-599-24582 | Sequence 24582, A |
| c 28 | 13 | 100.0 | 378 | 8 | US-10-425-115-48051 | Sequence 48051, A |
| c 29 | 13 | 100.0 | 386 | 8 | US-10-425-115-155338 | Sequence 155338, |
| c 30 | 13 | 100.0 | 395 | 4 | US-09-925-065A-182255 | Sequence 182255, |
| c 31 | 13 | 100.0 | 412 | 7 | US-10-424-599-92578 | Sequence 92578, A |
| c 32 | 13 | 100.0 | 413 | 4 | US-09-925-065A-210863 | Sequence 210863, |
| c 33 | 13 | 100.0 | 413 | 4 | US-09-925-065A-210864 | Sequence 210864, |
| c 34 | 13 | 100.0 | 415 | 7 | US-10-021-323-13591 | Sequence 13591, A |
| c 35 | 13 | 100.0 | 417 | 4 | US-09-925-065A-185779 | Sequence 185779, |
| c 36 | 13 | 100.0 | 421 | 7 | US-10-424-599-22487 | Sequence 22487, A |
| c 37 | 13 | 100.0 | 421 | 7 | US-10-424-599-132419 | Sequence 132419, |
| c 38 | 13 | 100.0 | 425 | 8 | US-10-425-115-174912 | Sequence 174912, |
| c 39 | 13 | 100.0 | 429 | 8 | US-10-425-115-173184 | Sequence 173184, |
| c 40 | 13 | 100.0 | 435 | 8 | US-10-677-254-1 | Sequence 1, Appl1 |
| c 41 | 13 | 100.0 | 435 | 8 | US-10-717-573-1 | Sequence 856288, |
| c 42 | 13 | 100.0 | 437 | 4 | US-09-925-065A-856288 | Sequence 856288, |
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| c 45 | 13 | 100.0 | 449 | 5 | US-10-027-632-42538 | Sequence 42538, A |

ALIGNMENTS

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Sequence 5, Application US/10677254
Publication No. US20040209279A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
TITLE OF INVENTION: HER, Guor Mour
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
FILE REFERENCE: 33151-188802
CURRENT APPLICATION NUMBER: US/10/677,254
CURRENT FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 13
TYPE: DNA
ORGANISM: Danio rerio
US-10-677-254-5

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Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAATAAACAGGG 13
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Sequence 5, Application US/10717573
Publication No. US20040209833A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
TITLE OF INVENTION: HER, Guor Mour
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
FILE REFERENCE: 33151-188802
CURRENT APPLICATION NUMBER: US/10/717,573
CURRENT FILING DATE: 2003-11-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 13
TYPE: DNA

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: April 1, 2006, 05:54:26 ; Search time 80.1483 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-4
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Sequence: 1 tccgataacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 17 | 14 | 100.0 | 446 | 11 | CR880560 Sub scrof |
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| 20 | 14 | 100.0 | 456 | 3 | BM497296 901150 AV |
| 21 | 14 | 100.0 | 462 | 1 | AW906100 EST342221 |
| 22 | 14 | 100.0 | 471 | 9 | AQ047435 cLM-1a4-u |

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| 34 | 14 | 100.0 | 537 | 11 | DE135963 Oryzias 1 |
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| 42 | 14 | 100.0 | 584 | 9 | AZ921335 1006029D1 |
| 43 | 14 | 100.0 | 587 | 3 | BU520198 BU520198 |
| 44 | 14 | 100.0 | 589 | 11 | DE053408 Oryzias 1 |
| 45 | 14 | 100.0 | 595 | 3 | BU532783 BU532783 |

ALIGNMENTS

RESULT 1
LOCUS BF991217/c
DEFINITION CM0-GN0162-271000-627-H01 GN0162 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF991217
VERSION BF991217.1 GI:12397542
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 203)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagel, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.O., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=CM0&c2=CM0-GN0162-271000-627-h01&c3=2000-10-27&c4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 203.
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-4

Perfect score: 14
Sequence: 1 tccgataacacaga 14

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapect 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: Geneseq22090s:*
13: Geneseq22100s:*
14: Geneseq22110s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 14 | 100.0 | 14 | ADT89053 | Adt89053 Zebrafish |
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| 4 | 14 | 100.0 | 435 | ADT89050 | Adt89050 Zebrafish |
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| 6 | 14 | 100.0 | 480 | ADT89079 | Adt89079 Zebrafish |
| 7 | 14 | 100.0 | 966 | ACA24900 | ACA24900 Prokaryot |
| 8 | 14 | 100.0 | 2033 | ADT08244 | Adt08244 Zebrafish |
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| 14 | 14 | 100.0 | 17 | ADT49791 | Adt49791 Human tum |
| 15 | 13 | 92.9 | 426 | ABZ31829 | Abz31829 Candida a |
| 16 | 13 | 92.9 | 441 | ADK61530 | Adk61530 Ovarian c |
| 17 | 13 | 92.9 | 575 | AA572226 | AA572226 DNA encod |
| 18 | 13 | 92.9 | 579 | ADF03348 | Adf03348 Bacterial |
| 19 | 13 | 92.9 | 677 | ACF67256 | ACF67256 Photornab |

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| 20 | 13 | 92.9 | 778 | 8 | ACA48582 | ACA48582 Prokaryot |
| 21 | 13 | 92.9 | 813 | 3 | AA708645 | AA708645 Fusarium |
| 22 | 13 | 92.9 | 813 | 3 | ADU52686 | ADU52686 Fusarium |
| 23 | 13 | 92.9 | 813 | 14 | AD290689 | Ad290689 Bacterial |
| 24 | 13 | 92.9 | 822 | 13 | ADT41711 | Adt41711 Bacterial |
| 25 | 13 | 92.9 | 957 | 8 | ACA52235 | ACA52235 Prokaryot |
| 26 | 13 | 92.9 | 1062 | 8 | ACA48942 | ACA48942 Prokaryot |
| 27 | 13 | 92.9 | 1065 | 8 | ACA52246 | ACA52246 Prokaryot |
| 28 | 13 | 92.9 | 1077 | 11 | ACH95736 | ACH95736 Klebsiell |
| 29 | 13 | 92.9 | 1104 | 6 | ABK75373 | Abk75373 Bacillus |
| 30 | 13 | 92.9 | 1383 | 11 | ACH98741 | ACH98741 Klebsiell |
| 31 | 13 | 92.9 | 1476 | 8 | ABT19416 | Abt19416 Aspergill |
| 32 | 13 | 92.9 | 1605 | 8 | ABT12126 | Abt12126 Aspergill |
| 33 | 13 | 92.9 | 1659 | 8 | ABT18822 | Abt18822 Aspergill |
| 34 | 13 | 92.9 | 1659 | 8 | ABT20638 | Abt20638 Aspergill |
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| 39 | 13 | 92.9 | 3084 | 6 | AB565016 | AB565016 Invertebr |
| 40 | 13 | 92.9 | 3455 | 2 | AAV81385 | AAV81385 Nucleic a |
| 41 | 13 | 92.9 | 3659 | 8 | ABT20042 | Abt20042 Aspergill |
| 42 | 13 | 92.9 | 3659 | 8 | ABT18228 | Abt18228 Aspergill |
| 43 | 13 | 92.9 | 3703 | 4 | ABT15078 | Abt15078 Drosophil |
| 44 | 13 | 92.9 | 3875 | 6 | ABL61897 | Ab161897 Colon ade |
| 45 | 13 | 92.9 | 3875 | 6 | ABN96818 | ABN96818 Gene #331 |

ALIGNMENTS

RESULT 1
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ID ADT08245 standard; DNA; 14 BP.

ADT08245;
13-JAN-2005 (first entry)

DE Zebrafish L-FABP upstream region HPH(1) binding site.

KM Zebrafish; ds; liver fatty acid binding protein; L-FABP;

KM liver regulatory element; LR; transgenic; HPH(1); HPH(2); HNF-1alpha;

KM HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;

KM liver development; liver disease; liver necrosis; liver cancer.

OS Danio rerio.

PN US2004209833-A1.

21-OCT-2004.

21-NOV-2003; 2003US-00717573.

16-APR-2003; 2003US-0463035P.

27-MAY-2003; 2003US-0473210P.

(WUJ/) WU J.

(HERG/) HER G M.

WU J, Her GM;

WPI; 2004-765481/75.

New isolated polynucleotide useful for generating transgenic fish such as zebrafish, comprises liver-specific expression control sequence that modulates expression of vertebrate liver fatty acid binding protein.

Claim 4, SEQ ID NO 4; 40pp: English.

The invention relates to an isolated polynucleotide comprising a liver-specific expression control sequence (LR) which modulates expression of a vertebrate liver fatty acid binding protein (L-FABP). Also included are a

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 83.2888 Seconds
(without alignments)
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Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataacacgaa 14

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

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Post-processing: Minimum Match 0%
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9: gb_ro :
10: gb_sts :
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12: gb_vl :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 14 | 100.0 | 1045 | AY494788 Banana bu |
| 5 | 14 | 100.0 | 2269 | BT002394 Arabidops |
| 6 | 14 | 100.0 | 2960 | AF512998 Danio rer |
| 7 | 14 | 100.0 | 3795 | CO850893 Sequence |
| 8 | 14 | 100.0 | 3795 | AK128090 Homo sapi |
| 9 | 14 | 100.0 | 15381 | CR388056 Zebrafish |
| 10 | 14 | 100.0 | 21024 | AE008736 Salmonell |
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| 12 | 14 | 100.0 | 53155 | BX511001 Zebrafish |
| 13 | 14 | 100.0 | 54620 | AC014122 Drosophila |
| 14 | 14 | 100.0 | 58988 | CR751229 Zebrafish |
| 15 | 14 | 100.0 | 71468 | AC151393 Ateleiix |
| 16 | 14 | 100.0 | 74832 | AP000455 Homo sapi |
| 17 | 14 | 100.0 | 80867 | BX908745 Zebrafish |
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| c 38 | 14 | 100.0 | 116929 | 14 | AL356001 | AL356001 Homo sapi |
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| c 40 | 14 | 100.0 | 121253 | 5 | CR352243 | CR352243 Zebrafish |
| c 41 | 14 | 100.0 | 126083 | 5 | CR339049 | CR339049 Zebrafish |
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| c 43 | 14 | 100.0 | 132833 | 5 | BX255928 | BX255928 Zebrafish |
| c 44 | 14 | 100.0 | 133128 | 5 | BX276083 | BX276083 Zebrafish |
| c 45 | 14 | 100.0 | 136155 | 5 | CR407548 | CR407548 Zebrafish |

ALIGNMENTS

| | | | | | |
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| LOCUS | Arabidopsis thaliana | transposon insertion | STS | GT_5.29319 | sequence |
| DEFINITION | CR379981 | 150 bp | DNA | linear | STS 24-MAR-2004 |
| ACCESSION | CR379981 | 150 bp | DNA | linear | STS 24-MAR-2004 |
| VERSION | CR379981.1 | GT:45726451 | | | |
| KEYWORDS | STS; STS, sequence tagged site. | | | | |
| SOURCE | Arabidopsis thaliana | | | | |
| ORGANISM | Arabidopsis thaliana | | | | |
| REFERENCE | 1 | Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M. | | | |
| AUTHORS | 1 | Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M. | | | |
| JOURNAL | 2 | (bases 1 to 150) | | | |
| TITLE | Submitted (22-MAR-2004) Clarke J.H., John Innes Centre, Colney | | | | |
| COMMENT | AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SW a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon. BSRG GARNET, ARIS project | | | | |
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OW nucleic - nucleic search, using SW model

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8902.774 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 26 | 12.4 | 88.6 | 231 | 3 | US-09-248-796A-11587 | Sequence 11587, A |
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| 30 | 12.4 | 88.6 | 390 | 3 | US-09-107-532A-775 | Sequence 775, App |
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ALIGNMENTS

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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7974
LENGTH: 1007
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-7974

Query Match Score 14: DB 3: Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-270-767-23256
Sequence 23256, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 23256
LENGTH: 1007
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-23256
Query Match Score 14: DB 3: Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

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OM nucleic - nucleic search, using BW model

Run on: April 1, 2006, 06:12:08 ; Search time 12.4363 Seconds
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Perfect score: 14
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US-09-925-065A-841694
Sequence 841694, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 841694

LENGTH: 483

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-841694

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCCGATAACAGAA 14

280 TCCGATAACAGAA 293

US-09-925-065A-32874

Application US/09925065A

Sequence 32874, Application US/09925065A

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 / Search time 16.322 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-4

Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA_Main*

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- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 14 | 100.0 | 405 | US-10-424-599-68519 | Sequence 68519, A |
| 4 | 14 | 100.0 | 412 | US-10-424-599-20783 | Sequence 20783, A |
| 5 | 14 | 100.0 | 435 | US-10-677-254-1 | Sequence 1, Appl1 |
| 6 | 14 | 100.0 | 435 | US-10-717-573-1 | Sequence 1, Appl1 |
| 7 | 14 | 100.0 | 480 | US-10-677-254-30 | Sequence 30, Appl1 |
| 8 | 14 | 100.0 | 480 | US-10-717-573-30 | Sequence 30, Appl1 |
| 9 | 14 | 100.0 | 483 | US-09-925-065A-841694 | Sequence 841694, A |
| 10 | 14 | 100.0 | 758 | US-09-925-065A-32874 | Sequence 32874, A |
| 11 | 14 | 100.0 | 758 | US-09-925-065A-32875 | Sequence 32875, A |
| 12 | 14 | 100.0 | 775 | US-10-424-599-64922 | Sequence 64922, A |
| 13 | 14 | 100.0 | 966 | US-10-282-122A-13770 | Sequence 12770, A |
| 14 | 14 | 100.0 | 2033 | US-10-677-254-3 | Sequence 12770, A |
| 15 | 14 | 100.0 | 2033 | US-10-717-573-3 | Sequence 3, Appl1 |
| 16 | 14 | 100.0 | 2783 | US-10-677-254-2 | Sequence 2, Appl1 |
| 17 | 14 | 100.0 | 2783 | US-10-717-573-2 | Sequence 2, Appl1 |
| 18 | 13 | 92.9 | 25 | US-10-719-956-424147 | Sequence 424147, A |
| 19 | 13 | 92.9 | 25 | US-10-956-157-53123 | Sequence 53123, A |
| 20 | 13 | 92.9 | 25 | US-10-956-157-53124 | Sequence 53124, A |
| 21 | 13 | 92.9 | 25 | US-10-956-157-53125 | Sequence 53125, A |
| 22 | 13 | 92.9 | 25 | US-10-956-157-53126 | Sequence 53126, A |
| 23 | 13 | 92.9 | 25 | US-10-956-157-137248 | Sequence 137248, A |

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| C 24 | 13 | 92.9 | 25 | 9 | US-10-843-527-90367 | Sequence 90367, A |
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| 26 | 13 | 92.9 | 201 | 8 | US-10-719-993-9873 | Sequence 9873, Ap |
| C 27 | 13 | 92.9 | 201 | 8 | US-10-719-993-32438 | Sequence 32438, A |
| C 28 | 13 | 92.9 | 201 | 8 | US-10-719-993-32440 | Sequence 32440, A |
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| 31 | 13 | 92.9 | 365 | 7 | US-10-437-965-42369 | Sequence 42369, A |
| 32 | 13 | 92.9 | 404 | 6 | US-10-062-674-579 | Sequence 579, App |
| 33 | 13 | 92.9 | 426 | 6 | US-10-032-585-6116 | Sequence 6116, Ap |
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| C 35 | 13 | 92.9 | 467 | 7 | US-10-424-599-36463 | Sequence 36463, A |
| C 36 | 13 | 92.9 | 530 | 7 | US-10-424-599-17599 | Sequence 17599, A |
| C 37 | 13 | 92.9 | 570 | 9 | US-10-450-763-8030 | Sequence 8030, Ap |
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| C 41 | 13 | 92.9 | 622 | 4 | US-09-925-065A-850883 | Sequence 850883, A |
| C 42 | 13 | 92.9 | 632 | 4 | US-09-925-065A-851180 | Sequence 851180, A |
| C 43 | 13 | 92.9 | 778 | 7 | US-10-282-122A-36452 | Sequence 36452, A |
| C 44 | 13 | 92.9 | 813 | 8 | US-10-653-047-1168 | Sequence 1168, Ap |
| C 45 | 13 | 92.9 | 822 | 6 | US-10-369-493-40149 | Sequence 40149, A |

ALIGNMENTS

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RESULT 1
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; Sequence 4, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDIN
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-4

Query Match      100.0%; Score 14; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. NO. 4.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGATTAACGAA 14
      |||||
      1 TCCGATTAACGAA 14

DB      1 TCCGATTAACGAA 14

RESULT 2
US-10-717-573-4
; Sequence 4, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDIN
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 14
; TYPE: DNA

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| C | 1 | 92 | 4.5 | 119036 | 8 | US-10-995-561-13314 | Sequence 13314, A |
| | 2 | 91.6 | 4.5 | 396 | 11 | US-11-250-759-53 | Sequence 53, A |
| C | 3 | 84 | 4.1 | 305312 | 8 | US-10-995-561-13236 | Sequence 13236, A |
| | 4 | 83.8 | 4.1 | 5501 | 8 | US-10-240-708-38 | Sequence 38, A |
| | 5 | 83.8 | 4.1 | 49979 | 8 | US-10-995-561-13443 | Sequence 13443, A |
| | 6 | 82.8 | 4.1 | 8961 | 8 | US-10-240-708-80 | Sequence 80, A |
| | 7 | 82.6 | 4.1 | 674 | 10 | US-10-301-480-532538 | Sequence 532538, A |
| | 8 | 82.6 | 4.1 | 674 | 10 | US-10-301-480-1145947 | Sequence 1145947, A |
| | 9 | 81.8 | 4.0 | 5662 | 8 | US-10-240-708-63 | Sequence 63, A |
| | 10 | 81.4 | 4.0 | 105550 | 8 | US-10-995-561-1235 | Sequence 1235, A |
| | 11 | 81.2 | 4.0 | 6070 | 8 | US-10-240-708-10 | Sequence 10, A |
| | 12 | 81 | 4.0 | 5152 | 8 | US-10-240-708-47 | Sequence 47, A |
| | 13 | 80.8 | 4.0 | 5844 | 8 | US-10-240-708-89 | Sequence 89, A |
| | 14 | 80.6 | 4.0 | 7001 | 14 | US-11-011-332A-103 | Sequence 103, A |
| | 15 | 80.4 | 4.0 | 28636 | 14 | US-11-011-332A-155 | Sequence 155, A |
| C | 16 | 80.4 | 4.0 | 687411 | 9 | US-10-330-772-26 | Sequence 26, A |
| C | 17 | 80.2 | 3.9 | 171486 | 14 | US-11-121-086-105 | Sequence 105, A |
| C | 18 | 80.2 | 3.9 | 173602 | 14 | US-11-121-086-55 | Sequence 25, A |

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| | Matches | 256; | Conservative | 0; | Mismatches 255; Indels 1; Gaps 1; |
| Oy | 1066 | TTTATTAAGATTATTTATTTATTTATTTATTTATCTATTTATTTATTTAGTGCT | 11225 | | |
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| Oy | 1126 | TTATTTATCTCGAGATCAGCCGTGGCCTTTTCATTATTTAAATTTTAAATTTA | 11858 | | |
| Dp | 31661 | TATATATTTATATATATATATATATCATAT-TTATATATATATATATCTATTTTATATATA | 31660 | | |
| Oy | 1186 | ATTTCCTTTATTTTTTTTTTATTTTTTTATTTTATTTACAGTCGACCAATACT | 1245 | | |
| Dp | 31602 | TTTATATATTTTATATATATATATCTTATTTTATATATATTTTATATATATATATATAT | 3154 | | |
| Oy | 1246 | GACCTAAAACCTCGAGATCATGTCTATGCATTTTATTTTATTTTCATTTTATAT | 1305 | | |

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 2370.19 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-3

Perfect score: 2033
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 7 | 480 | 23.6 | 480 | 8 | US-10-677-254-30 |
| 8 | 480 | 23.6 | 480 | 8 | US-10-717-573-30 |
| 9 | 435 | 21.4 | 435 | 8 | US-10-677-254-1 |
| 10 | 435 | 21.4 | 435 | 8 | US-10-717-573-1 |
| 11 | 220.2 | 10.8 | 13382 | 8 | US-10-612-594-4 |
| 12 | 198.6 | 9.8 | 3003 | 9 | US-10-511-362-9 |
| 13 | 193.2 | 9.5 | 5563 | 5 | US-10-136-734-26 |
| 14 | 185.6 | 9.1 | 7495 | 7 | US-10-742-828-5 |
| 15 | 185.6 | 9.1 | 7508 | 7 | US-10-742-828-4 |
| 16 | 184.8 | 9.1 | 13382 | 8 | US-10-612-594-4 |
| 17 | 126.4 | 6.2 | 1062 | 8 | US-10-425-115-120013 |
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| 22 | 118.4 | 5.8 | 1214 | 7 | US-10-424-599-102083 |
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| 24 | 117.8 | 5.8 | 6109 | 6 | US-10-311-455-299 | Sequence 299, App |
| 25 | 117.8 | 5.8 | 6109 | 7 | US-10-221-613-33 | Sequence 33, App1 |
| 26 | 117.4 | 5.8 | 17934 | 6 | US-10-311-455-1692 | Sequence 1692, App |
| 27 | 117.2 | 5.8 | 6419 | 6 | US-10-311-455-240 | Sequence 240, App |
| 28 | 117.2 | 5.8 | 71843 | 9 | US-10-488-292-3 | Sequence 3, App1 |
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| 30 | 116.2 | 5.7 | 6668 | 6 | US-10-311-455-1670 | Sequence 1670, App |
| 31 | 115.8 | 5.7 | 921 | 8 | US-10-425-115-13810 | Sequence 3870, App |
| 32 | 115.8 | 5.7 | 1204 | 7 | US-10-437-963-77858 | Sequence 77858, App |
| 33 | 115.8 | 5.7 | 16033 | 6 | US-10-311-455-1377 | Sequence 1377, App |
| 34 | 115.4 | 5.7 | 1039 | 8 | US-10-425-115-58802 | Sequence 58802, App |
| 35 | 115.2 | 5.7 | 803 | 7 | US-10-437-963-72176 | Sequence 72176, App |
| 36 | 114.2 | 5.6 | 996 | 8 | US-10-425-115-151933 | Sequence 151933, App |
| 37 | 114 | 5.6 | 6286 | 7 | US-10-221-714A-313 | Sequence 313, App |
| 38 | 113.8 | 5.6 | 6145 | 6 | US-10-311-455-945 | Sequence 945, App |
| 39 | 113.8 | 5.6 | 7597 | 6 | US-10-311-455-986 | Sequence 986, App |
| 40 | 113.6 | 5.6 | 739 | 8 | US-10-425-115-55020 | Sequence 55020, App |
| 41 | 113.6 | 5.6 | 1243 | 8 | US-10-425-115-172717 | Sequence 172717, App |
| 42 | 113.2 | 5.6 | 1300 | 7 | US-10-668-749A-1 | Sequence 1, App1 |
| 43 | 113.2 | 5.6 | 1121 | 8 | US-10-425-115-15706 | Sequence 115706, App |
| 44 | 112.6 | 5.5 | 1004 | 8 | US-10-425-115-81106 | Sequence 81106, App |
| 45 | 112.4 | 5.5 | 3683 | 8 | US-10-473-126-339 | Sequence 339, App |

ALIGNMENTS

RESULT 1
US-10-677-254-3
Sequence 3, Application US/10677254
Publication NO. US20040209279A1
GENERAL INFORMATION:
APPLICANT: WU, Jen-Leih
APPLICANT: HRR, Guor Mour
TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATY ACID BINDING
TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
FILE REFERENCE: 33151-188802
CURRENT APPLICATION NUMBER: US/10/677,254
CURRENT FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 2033
TYPE: DNA
ORGANISM: Danio rerio
US-10-677-254-3

| Query Match | 100.0% | Score 2033 | DB 8 | Length 2033 |
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| Best Local Similarity | 100.0% | Pred. No. 1.6e-308 | Mismatches 0 | Indels 0 |
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| Qy | 61 | TTTTGATAGTCTACAGAACCAACATCGGTATPACATGACTTGCTTAATTAACCTTAAC | 120 | Sequence 1692, App |
| Db | 61 | TTTTGATAGTCTACAGAACCAACATCGGTATPACATGACTTGCTTAATTAACCTTAAC | 120 | Sequence 240, App |
| Qy | 121 | TGCTGATTAATGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 180 | Sequence 3, App1 |
| Db | 121 | TGCTGATTAATGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 180 | Sequence 2331, App |
| Qy | 181 | GTCGCTTGAAGATATCTAGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 240 | Sequence 1670, App |
| Db | 181 | GTCGCTTGAAGATATCTAGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 240 | Sequence 3870, App |
| Qy | 241 | ATCAGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 300 | Sequence 77858, App |
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| Db | 301 | AGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 360 | Sequence 72176, App |

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 1663.92 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-3

Perfect score: 2033

Sequence: 1 gtttatactagtttatacgc.....gttgagctctccagaagac 2033

Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 31 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 32 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 33 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 34 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 35 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 36 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 37 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 38 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 39 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 40 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 41 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 42 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 43 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 44 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |
| 45 | 2033 | 100.0 | 2033 | 13 | ADT08244 Zebrafish |

| | | | | | | | |
|---|----|-------|-----|-------|----|----------|--------------------|
| c | 20 | 122 | 6.0 | 612 | 14 | ACT64894 | ACT64894 M. xanthu |
| c | 21 | 121.4 | 6.0 | 14006 | 6 | ABL33958 | ABL33958 Human imm |
| c | 22 | 119.2 | 5.9 | 2520 | 12 | ADJ48201 | ADJ48201 Maize o1l |
| c | 23 | 117.8 | 5.8 | 446 | 8 | ABX38235 | ABX38235 Bovine ES |
| c | 24 | 117.8 | 5.8 | 6109 | 6 | ABL32326 | ABL32326 Human imm |
| c | 25 | 117.8 | 5.8 | 6109 | 6 | AA661077 | AA661077 Human gen |
| c | 26 | 117.6 | 5.8 | 700 | 10 | ACD92384 | ACD92384 Human col |
| c | 27 | 117.6 | 5.8 | 6644 | 2 | AXX33181 | AXX33181 Base sequ |
| c | 28 | 117.6 | 5.8 | 7372 | 2 | AXX33182 | AXX33182 Base sequ |
| c | 29 | 117.6 | 5.8 | 7797 | 2 | AXX33180 | AXX33180 Compox vi |
| c | 30 | 117.6 | 5.8 | 7996 | 2 | AXX33184 | AXX33184 Base sequ |
| c | 31 | 117.4 | 5.8 | 17934 | 6 | ABL33719 | ABL33719 Human imm |
| c | 32 | 117.2 | 5.8 | 6419 | 6 | ABL32667 | ABL32667 Human imm |
| c | 33 | 117.2 | 5.8 | 71843 | 8 | ACC79619 | ACC79619 Zebrafish |
| c | 34 | 116.4 | 5.7 | 12237 | 6 | ABL34358 | ABL34358 Human imm |
| c | 35 | 116.2 | 5.7 | 6668 | 6 | ABL33697 | ABL33697 Human imm |
| c | 36 | 115.8 | 5.7 | 16033 | 6 | ABL33404 | ABL33404 Human imm |
| c | 37 | 114 | 5.6 | 6286 | 4 | AA546591 | AA546591 Tumour su |
| c | 38 | 113.8 | 5.6 | 6145 | 6 | ABL32972 | ABL32972 Human imm |
| c | 39 | 113.8 | 5.6 | 7597 | 6 | ABL33013 | ABL33013 Human imm |
| c | 40 | 113.6 | 5.6 | 1000 | 12 | ADQ62833 | ADQ62833 Homopoly- |
| c | 41 | 113.6 | 5.6 | 1000 | 12 | ADQ62832 | ADQ62832 Homopoly- |
| c | 42 | 113.6 | 5.6 | 1300 | 12 | ADP85917 | ADP85917 Synthetic |
| c | 43 | 112.4 | 5.5 | 3683 | 8 | AB210199 | AB210199 Haematopo |
| c | 44 | 112 | 5.5 | 556 | 6 | ABQ36997 | ABQ36997 Oligonuc |
| c | 45 | 112 | 5.5 | 556 | 6 | ABQ36996 | ABQ36996 Oligonuc |

ALIGNMENTS

| | | |
|----------|---|----------------------------------|
| RESULT 1 | ADT08244 | ADT08244 standard; DNA; 2033 BP. |
| XX | ADT08244; | |
| XX | 13-JAN-2005 (first entry) | |
| DT | 13-JAN-2005 | |
| XX | Zebrafish L-FABP upstream region -2033 to -1. | |
| XX | Zebrafish; ds; liver fatty acid binding protein; L-FABP; | |
| KW | liver regulatory element; LR; transgenic; HPH(1); HPH(2); HNF-1alpha; | |
| KW | HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP; | |
| KW | liver development; liver disease; liver necrosis; liver cancer. | |
| XX | Danio rerio. | |
| OS | Danio rerio. | |
| XX | US2004209833-A1. | |
| PN | US2004209833-A1. | |
| XX | 21-OCT-2004. | |
| PD | 21-OCT-2004. | |
| XX | 21-NOV-2003; 2003US-00717573. | |
| PF | 21-NOV-2003; 2003US-00717573. | |
| XX | 16-APR-2003; 2003US-0463035P. | |
| PR | 27-MAY-2003; 2003US-0473210P. | |
| XX | (WUJ/) WU J. | |
| PA | (HERG/) HER G. M. | |
| XX | Wu J, Her GM; | |
| PI | Wu J, Her GM; | |
| XX | WPI, 2004-765481/75. | |
| DR | WPI, 2004-765481/75. | |
| XX | New isolated polynucleotide useful for generating transgenic fish such as | |
| PT | zebrafish, comprises liver-specific expression control sequence that | |
| XX | modulates expression of vertebrate liver fatty acid binding protein. | |
| XX | Claim 11; SEQ ID NO 3; 40pp; English. | |
| PS | The invention relates to an isolated polynucleotide comprising a liver- | |
| XX | specific expression control sequence (LR) which modulates expression of a | |
| CC | vertebrate liver fatty acid binding protein (L-FABP). Also included are a | |

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 12094.7 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-3

Perfect score: 2033

Sequence: 1 gtttcaatagctttatgc.....gttgagcttcacagaagc 2033

Scoring table: IDENTITY NTC

Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBml.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pac.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vl.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|--------|--------------------|--------|---------------------|
| 1 | 2033 | 100.0 | 2960 | AF512998 Danio rer |
| 2 | 1164.6 | 57.3 | 178271 | CR293507 zebrafish |
| 3 | 306.6 | 15.1 | 80017 | AL845372 zebrafish |
| 4 | 295.4 | 14.5 | 150673 | CR361557 Danio rer |
| 5 | 295 | 14.5 | 85762 | CR388368 zebrafish |
| 6 | 274.4 | 13.5 | 223535 | CR376787 Danio rer |
| 7 | 273 | 13.4 | 192644 | CR3762383 zebrafish |
| 8 | 272.6 | 13.4 | 173481 | AL928671 zebrafish |
| 9 | 268.6 | 13.2 | 110000 | CR753903 Danio rer |
| 10 | 268.4 | 13.2 | 222875 | CR848050 Danio rer |
| 11 | 265.6 | 13.1 | 169046 | AL928828 zebrafish |
| 12 | 265.2 | 13.0 | 170625 | CR854833 Danio rer |
| 13 | 264.8 | 13.0 | 109430 | CT009663 Danio rer |
| 14 | 264.8 | 13.0 | 149742 | CR382286 zebrafish |
| 15 | 264.8 | 13.0 | 169758 | CR936240 zebrafish |
| 16 | 264.4 | 13.0 | 117304 | BX470100 zebrafish |
| 17 | 264.4 | 13.0 | 202883 | BX470165 Danio rer |
| 18 | 263.8 | 13.0 | 143812 | BX957262 zebrafish |

| | | | | | | |
|----|-------|------|--------|----|----------|--------------------|
| 19 | 263.8 | 13.0 | 172321 | 5 | AL844171 | AL844171 zebrafish |
| 20 | 263.2 | 12.9 | 304914 | 14 | BX942830 | BX942830 Danio rer |
| 21 | 262.8 | 12.9 | 165603 | 5 | BX548250 | BX548250 zebrafish |
| 22 | 261 | 12.8 | 172841 | 14 | AL928708 | AL928708 Danio rer |
| 23 | 260.2 | 12.8 | 179240 | 5 | BX005309 | BX005309 zebrafish |
| 24 | 259.8 | 12.8 | 156150 | 5 | BX322540 | BX322540 zebrafish |
| 25 | 259.8 | 12.8 | 167345 | 5 | BX004771 | BX004771 zebrafish |
| 26 | 259 | 12.7 | 190968 | 5 | BX465217 | BX465217 zebrafish |
| 27 | 258.8 | 12.7 | 185806 | 14 | CR933100 | CR933100 Danio rer |
| 28 | 258.6 | 12.7 | 152840 | 5 | AL732567 | AL732567 zebrafish |
| 29 | 258.4 | 12.7 | 200760 | 5 | AL928872 | AL928872 zebrafish |
| 30 | 258.2 | 12.7 | 182255 | 14 | CR938723 | CR938723 Danio rer |
| 31 | 257.8 | 12.7 | 185855 | 14 | CR759734 | CR759734 zebrafish |
| 32 | 257.8 | 12.7 | 191769 | 14 | CR933561 | CR933561 Danio rer |
| 33 | 257.8 | 12.7 | 192592 | 5 | AL929096 | AL929096 zebrafish |
| 34 | 257.4 | 12.7 | 136156 | 14 | CR847502 | CR847502 Danio rer |
| 35 | 257.4 | 12.7 | 148815 | 14 | CR376750 | CR376750 Danio rer |
| 36 | 257.2 | 12.7 | 185384 | 14 | CR391914 | CR391914 Danio rer |
| 37 | 257.2 | 12.7 | 203371 | 14 | AC139623 | AC139623 Danio rer |
| 38 | 257 | 12.6 | 151770 | 14 | CR925754 | CR925754 Danio rer |
| 39 | 257 | 12.6 | 289569 | 14 | CR382321 | CR382321 Danio rer |
| 40 | 256.8 | 12.6 | 105764 | 5 | CR385077 | CR385077 zebrafish |
| 41 | 256.8 | 12.6 | 153159 | 14 | CR936337 | CR936337 Danio rer |
| 42 | 256.6 | 12.6 | 162436 | 5 | AL929535 | AL929535 zebrafish |
| 43 | 256 | 12.6 | 149630 | 14 | CR628386 | CR628386 Danio rer |
| 44 | 256 | 12.6 | 165139 | 14 | CR925756 | CR925756 Danio rer |
| 45 | 256 | 12.6 | 201151 | 14 | BX511097 | BX511097 Danio rer |

ALIGNMENTS

| | | | | | |
|------------|--|---|-----|--------|-----------------|
| RESULT 1 | AF512998 | 2960 bp | DNA | linear | VRT 10-JUN-2003 |
| LOCUS | Danio rerio | liver-type fatty acid binding protein gene, partial | | | |
| DEFINITION | cds. | | | | |
| ACCESSION | AF512998 | | | | |
| VERSION | AF512998.1 | GI:21314558 | | | |
| KEYWORDS | | | | | |
| SOURCE | Danio rerio (zebrafish) | | | | |
| ORGANISM | Danio rerio | | | | |
| REFERENCE | Her, G.M., Yeh, Y.H. and Wu, J.L. | | | | |
| AUTHORS | Her, G.M., Yeh, Y.H. and Wu, J.L. | | | | |
| TITLE | 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish | | | | |
| JOURNAL | Dev. Dyn. 227 (3), 347-356 (2003) | | | | |
| PUBMED | 12815620 | | | | |
| REFERENCE | 2 (bases 1 to 2960) | | | | |
| AUTHORS | Her, G.M. and Wu, J.-L. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan | | | | |
| FEATURES | Location/Qualifiers | | | | |
| SOURCE | 1..2960 | | | | |
| FEATURES | /organism="Danio rerio" | | | | |
| FEATURES | /mol_type="genomic DNA" | | | | |
| FEATURES | /db_xref="taxon:7955" | | | | |
| FEATURES | <2784..>2960 | | | | |
| FEATURES | /product="liver-type fatty acid binding protein" | | | | |
| FEATURES | /note="Lifabp; small cytosolic protein involved in lipid transport and metabolism" | | | | |
| FEATURES | /codon_start=1 | | | | |
| FEATURES | /product="liver-type fatty acid binding protein" | | | | |
| FEATURES | /protein_id="BA047005.1" | | | | |
| FEATURES | /db_xref="GI:21314559" | | | | |
| FEATURES | /translation="MAFGTWOVYAQENYEFRLAISLPEVTKLAKQKPVETIQNG | | | | |
| FEATURES | GSDFITRSKTPGKTV" | | | | |

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 2277.76 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-2

Perfect score: 2783
Sequence: 1 gcgcgaatgatccaact.....gttcagctctccagaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_21:*
2: geneseq1980s:*
3: geneseq1990s:*
4: geneseq2000s:*
5: geneseq2001as:*
6: geneseq2001bs:*
7: geneseq2002as:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*
14: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 2783 | 100.0 | 2783 | ADT08243 | Adt08243 Zebrafish |
| 2 | 2783 | 100.0 | 2783 | ADT89051 | Adt89051 Zebrafish |
| 3 | 2783 | 100.0 | 2960 | ADT89080 | Adt89080 Zebrafish |
| 4 | 2033 | 73.1 | 2033 | ADT08244 | Adt08244 Zebrafish |
| 5 | 2033 | 73.1 | 2033 | ADT89052 | Adt89052 Zebrafish |
| 6 | 863 | 31.0 | 1086 | ADT89026 | Adt89026 Zebrafish |
| 7 | 863 | 31.0 | 1086 | ADT89076 | Adt89076 Zebrafish |
| 8 | 480 | 17.2 | 480 | ADT08271 | Adt08271 Zebrafish |
| 9 | 480 | 17.2 | 480 | ADT89079 | Adt89079 Zebrafish |
| 10 | 435 | 15.6 | 435 | ADT08242 | Adt08242 Zebrafish |
| 11 | 435 | 15.6 | 435 | ADT89050 | Adt89050 Zebrafish |
| 12 | 348 | 12.5 | 71843 | ACC79619 | Acc79619 Zebrafish |
| 13 | 260.4 | 9.4 | 78064 | ADSI17402 | Adsi17402 Nucleicid |
| 14 | 257.6 | 9.3 | 78064 | ADSI17402 | Adsi17402 Nucleicid |
| 15 | 251.4 | 9.0 | 13382 | ADM44488 | Adm44488 Zebrafish |
| 16 | 217.6 | 7.8 | 13382 | ADM44488 | Adm44488 Zebrafish |
| 17 | 207.2 | 7.4 | 3003 | ADT18692 | Adt18692 Zebrafish |
| 18 | 206.8 | 7.4 | 7495 | ADR30815 | Adr30815 Zebrafish |
| 19 | 206.8 | 7.4 | 7508 | ADR30814 | Adr30814 Zebrafish |

| | | | | | | |
|---|----|-------|-----|-------|----|----------|
| C | 20 | 200.8 | 7.2 | 5563 | 2 | AAx08941 |
| C | 21 | 122 | 4.4 | 612 | 14 | ACI64894 |
| C | 22 | 121.4 | 4.4 | 14006 | 6 | ABL33958 |
| C | 23 | 119.2 | 4.3 | 2520 | 12 | ADJ48201 |
| C | 24 | 117.8 | 4.2 | 446 | 8 | ABX38235 |
| C | 25 | 117.8 | 4.2 | 6109 | 6 | ABL32336 |
| C | 26 | 117.8 | 4.2 | 6109 | 6 | ABG61077 |
| C | 27 | 117.6 | 4.2 | 700 | 10 | ACD92384 |
| C | 28 | 117.6 | 4.2 | 6644 | 2 | AAx33181 |
| C | 29 | 117.6 | 4.2 | 7372 | 2 | AAx33182 |
| C | 30 | 117.6 | 4.2 | 7797 | 2 | AAx33180 |
| C | 31 | 117.6 | 4.2 | 7996 | 2 | AAx33184 |
| C | 32 | 117.4 | 4.2 | 17934 | 6 | ABL33719 |
| C | 33 | 117.2 | 4.2 | 6419 | 6 | ABL32267 |
| C | 34 | 117.2 | 4.2 | 71843 | 6 | ACCT9619 |
| C | 35 | 116.4 | 4.2 | 12237 | 6 | ABL34358 |
| C | 36 | 116.2 | 4.2 | 6668 | 6 | ABL33697 |
| C | 37 | 115.8 | 4.2 | 16033 | 6 | ABL33404 |
| C | 38 | 114 | 4.1 | 6286 | 4 | AAx46591 |
| C | 39 | 113.8 | 4.1 | 7597 | 6 | ABL32972 |
| C | 40 | 113.8 | 4.1 | 1000 | 12 | ADG62833 |
| C | 41 | 113.6 | 4.1 | 1300 | 12 | ADP85917 |
| C | 42 | 113.6 | 4.1 | 1300 | 12 | ADP85917 |
| C | 43 | 113.6 | 4.0 | 8056 | 8 | ABZ10246 |
| C | 44 | 112.6 | 4.0 | 3683 | 8 | ABZ10199 |
| C | 45 | 112.4 | 4.0 | | | |

ALIGNMENTS

| | | |
|----------|---|----------------------------------|
| RESULT 1 | ADT08243 | ADT08243 standard; DNA; 2783 BP. |
| ID | ADT08243 | |
| AC | ADT08243; | |
| DT | 13-JAN-2005 | (first entry) |
| DE | Zebrafish L-FABP upstream region plus some coding region. | |
| FW | Zebrafish; de; liver fatty acid binding protein; L-FABP; | |
| KW | liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha; | |
| KW | HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP; | |
| KW | liver development; liver disease; liver necrosis; liver cancer; promoter. | |
| OS | Danio rerio. | |
| XX | US2004209833-A1. | |
| XX | 21-OCT-2004. | |
| XX | 21-NOV-2003; 2003US-00717573. | |
| XX | 16-APR-2003; 2003US-0463035P. | |
| XX | 27-MAY-2003; 2003US-0473210P. | |
| XX | (WUJ/) WU J. | |
| XX | (HERG/) HER G M. | |
| XX | WU J, Her GM; | |
| XX | WPI, 2004-765481/75. | |
| XX | New isolated polynucleotide useful for generating transgenic fish such as | |
| XX | zebrafish, comprises liver-specific expression control sequence that | |
| XX | modulates expression of vertebrate liver fatty acid binding protein. | |
| XX | Claim 10; SEQ ID NO 2; 40pp; English. | |
| XX | The invention relates to an isolated polynucleotide comprising a liver- | |
| XX | specific expression control sequence (LR) which modulates expression of a | |
| XX | vertebrate liver fatty acid binding protein (L-FABP). Also included are a | |

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 16556.6 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-2

Perfect score: 2783
Sequence: 1 gctgaataatgattcaaac.....gtcgaactctccagaagc 2783

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 2783 | 100.0 | 2960 | AF512998 | Danio rer |
| 2 | 1828 | 65.7 | 178271 | CR293507 | CR293507 Zebrafish |
| 3 | 521.8 | 18.7 | 132182 | CR848746 | CR848746 Danio rer |
| 4 | 520 | 18.7 | 166638 | CR548631 | CR548631 Danio rer |
| 5 | 518 | 18.6 | 159232 | BX119923 | BX119923 Zebrafish |
| 6 | 515.8 | 18.5 | 195837 | AL953868 | AL953868 Danio rer |
| 7 | 512.6 | 18.4 | 160252 | CR847928 | CR847928 Zebrafish |
| 8 | 512.4 | 18.4 | 168638 | CR548631 | CR548631 Danio rer |
| 9 | 512.4 | 18.4 | 178075 | CR847790 | CR847790 Danio rer |
| 10 | 512.4 | 18.4 | 182355 | CR938723 | CR938723 Danio rer |
| 11 | 510.4 | 18.3 | 73696 | AL772143 | AL772143 Zebrafish |
| 12 | 510.4 | 18.3 | 85075 | BX681415 | BX681415 Danio rer |
| 13 | 510.4 | 18.3 | 162045 | CR318660 | CR318660 Zebrafish |
| 14 | 510.2 | 18.3 | 216472 | CR356243 | CR356243 Zebrafish |
| 15 | 508 | 18.3 | 112811 | BX005301 | BX005301 Zebrafish |
| 16 | 507.8 | 18.2 | 169760 | BX511310 | BX511310 Zebrafish |
| 17 | 507.8 | 18.2 | 201525 | AL954172 | AL954172 Zebrafish |
| 18 | 507.2 | 18.2 | 187161 | BX088526 | BX088526 Zebrafish |

| | | | | | | | |
|---|----|-------|------|--------|----|------------|---------------------|
| c | 19 | 506.4 | 18.2 | 74150 | 14 | BX27093 | Danio rer |
| c | 20 | 506.4 | 18.2 | 152488 | 14 | CR407597 | CR407597 Danio rer |
| c | 21 | 505.4 | 18.2 | 145294 | 5 | CR354539 | CR354539 Zebrafish |
| c | 22 | 505.4 | 18.2 | 178457 | 5 | AL935031 | AL935031 Zebrafish |
| c | 23 | 504.4 | 18.1 | 202138 | 5 | BX004991 | BX004991 Zebrafish |
| c | 24 | 504 | 18.1 | 149598 | 5 | BX957346 | BX957346 Zebrafish |
| c | 25 | 504 | 18.1 | 157294 | 14 | CR848023 | CR848023 Danio rer |
| c | 26 | 503.4 | 18.1 | 178425 | 5 | CR354429 | CR354429 Zebrafish |
| c | 27 | 502.6 | 18.1 | 169310 | 5 | BX323461 | BX323461 Zebrafish |
| c | 28 | 502.4 | 18.1 | 146348 | 5 | CR548627 | CR548627 Zebrafish |
| c | 29 | 502.2 | 18.0 | 217527 | 14 | CR394525 | CR394525 Danio rer |
| c | 30 | 501.4 | 18.0 | 176982 | 5 | AL7732610 | AL7732610 Zebrafish |
| c | 31 | 501.4 | 18.0 | 232594 | 5 | BX005006 | BX005006 Zebrafish |
| c | 32 | 501.2 | 18.0 | 107132 | 5 | BX255941 | BX255941 Zebrafish |
| c | 33 | 500.8 | 18.0 | 158133 | 5 | BX000348 | BX000348 Zebrafish |
| c | 34 | 499.2 | 17.9 | 178243 | 5 | BX248504 | BX248504 Zebrafish |
| c | 35 | 498 | 17.9 | 155693 | 14 | CR524823 | CR524823 Danio rer |
| c | 36 | 497.2 | 17.9 | 149008 | 14 | BX296524 | BX296524 Danio rer |
| c | 37 | 497.2 | 17.9 | 149329 | 14 | BX511217 | BX511217 Danio rer |
| c | 38 | 497 | 17.9 | 110000 | 14 | AL954295_2 | Continuation (3 of |
| c | 39 | 497 | 17.9 | 110000 | 14 | AL954295_5 | Continuation (6 of |
| c | 40 | 497 | 17.9 | 130060 | 5 | AL929217 | Zebrafish |
| c | 41 | 497 | 17.9 | 141118 | 14 | CR391998 | Danio rer |
| c | 42 | 495.8 | 17.8 | 127576 | 5 | AC144824 | Danio rer |
| c | 43 | 495.2 | 17.8 | 137166 | 5 | AL929566 | AL929566 Zebrafish |
| c | 44 | 495.2 | 17.8 | 166869 | 14 | BX005359 | Danio rer |
| c | 45 | 495 | 17.8 | 205568 | 5 | BX470184 | Zebrafish |

ALIGNMENTS

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| LOCUS | AF512998 | | | | |
| DEFINITION | Danio rerio liver-type fatty acid binding protein gene, partial cds. | | | | |
| ACCESSION | AF512998 | | | | |
| VERSION | AF512998.1 | GI:21314558 | | | |
| KEYWORDS | | | | | |
| SOURCE | Danio rerio (zebrafish) | | | | |
| ORGANISM | Danio rerio | | | | |
| REFERENCE | Her, G.M., Yen, Y.H. and Wu, J.L. | | | | |
| AUTHORS | 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish | | | | |
| TITLE | Dev. Dyn. 227 (3), 347-356 (2003) | | | | |
| JOURNAL | PUBMED | | | | |
| REFERENCE | 2 (bases 1 to 2960) | | | | |
| AUTHORS | Her, G.M. and Wu, J.L. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan | | | | |
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Run on: April 1, 2006, 06:06:01 ; Search time 344.58 Seconds
(without alignments)
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Title: US-10-717-573-2

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 5 | 863 | 31.0 | 1086 | US-10-677-254-27 | Sequence 27, Appl1 |
| 6 | 863 | 31.0 | 1086 | US-10-717-573-27 | Sequence 27, Appl1 |
| 7 | 480 | 17.2 | 480 | US-10-677-254-30 | Sequence 30, Appl1 |
| 8 | 480 | 17.2 | 480 | US-10-717-573-30 | Sequence 30, Appl1 |
| 9 | 435 | 15.6 | 435 | US-10-677-254-1 | Sequence 1, Appl1 |
| 10 | 435 | 15.6 | 435 | US-10-717-573-1 | Sequence 1, Appl1 |
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| 14 | 217.6 | 7.8 | 13382 | US-10-612-594-4 | Sequence 4, Appl1 |
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| 16 | 206.8 | 7.4 | 7495 | US-10-742-828-5 | Sequence 5, Appl1 |
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| | 29 | 117.2 | 4.2 | 6419 | 6 | US-10-311-455-240 | Sequence 240, Appl1 |
| C | 30 | 117.2 | 4.2 | 71843 | 9 | US-10-488-292-3 | Sequence 3, Appl1 |
| | 31 | 116.4 | 4.2 | 12227 | 6 | US-10-311-455-2331 | Sequence 2331, Ap |
| | 32 | 116.2 | 4.2 | 6668 | 6 | US-10-311-455-1670 | Sequence 1670, Ap |
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ALIGNMENTS

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| Sequence 2, Application US/10677254 | | | | | | | | | |
| Publication No. US20040209279A1 | | | | | | | | | |
| GENERAL INFORMATION: | | | | | | | | | |
| APPLICANT: HER, Jen-Leih | | | | | | | | | |
| TITLE OF INVENTION: MU, Jen-Leih | | | | | | | | | |
| TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING | | | | | | | | | |
| FILE REFERENCE: 33151-168802 | | | | | | | | | |
| CURRENT APPLICATION NUMBER: US/10/677, 254 | | | | | | | | | |
| CURRENT FILING DATE: 2003-10-03 | | | | | | | | | |
| NUMBER OF SEQ ID NOS: 30 | | | | | | | | | |
| SOFTWARE: PatentIn version 3.2 | | | | | | | | | |
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| LENGTH: 2783 | | | | | | | | | |
| TYPE: DNA | | | | | | | | | |
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| US-10-677-254-2 | | | | | | | | | |
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| Best Local Similarity 100.0%; Pred. No. 0; | | | | | | | | | |
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ALIGNMENTS

RESULT 1

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/ Publication No. US20050266459A1
/ GENERAL INFORMATION:
/ APPLICANT: POULSEN, TIM S.
/ APPLICANT: NIELSEN, KIRSTEN V.
/ TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
/ FILE REFERENCE: 09138,6000-00000
/ CURRENT APPLICATION NUMBER: US/11/121,086
/ CURRENT FILING DATE: 2005-05-04
/ PRIOR APPLICATION NUMBER: 60/567,570
/ PRIOR FILING DATE: 2004-05-04
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn version 3.3
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ JS-11-121-086-96

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| QY | 225 | AATTAACAGGGGGCTAATTAATTTAAGGGTTAATAATTTCTGATTCGCAAAAAAATGA | 284 |
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| Db | 43465 | CATATACCTTTATATATTAATTAATCACTATATATTTATATATTTTAATCATATATTTAATA | 43524 |

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OM nucleic - nucleic search, using SW model

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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| C 19 | 44.4 | 10.2 | US-09-641-638-651 | Sequence 651, App |
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| C 23 | 44.4 | 10.2 | US-09-949-016-17475 | Sequence 17475, A |
| C 24 | 44.4 | 10.2 | US-09-949-016-12639 | Sequence 12639, A |

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| C 27 | 44.2 | 10.2 | 701 | 3 | US-08-998-416-701 | Sequence 701, App |
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| C 31 | 44.2 | 10.2 | 828 | 3 | US-08-998-416-538 | Sequence 538, App |
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| C 33 | 43.8 | 10.1 | 6881 | 3 | US-09-949-016-17181 | Sequence 17181, A |
| C 34 | 43.8 | 10.1 | 15220 | 3 | US-09-949-016-16311 | Sequence 16311, A |
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| C 36 | 43.6 | 10.0 | 96922 | 3 | US-09-949-016-17061 | Sequence 17061, A |
| C 37 | 43.4 | 10.0 | 696 | 3 | US-09-248-796A-11043 | Sequence 11043, A |
| C 38 | 43.4 | 10.0 | 782 | 3 | US-08-998-416-224 | Sequence 224, App |
| C 39 | 43.2 | 9.9 | 32721 | 3 | US-09-949-016-14100 | Sequence 14100, A |
| C 40 | 43.2 | 9.9 | 45138 | 3 | US-09-949-016-11027 | Sequence 13027, A |
| C 41 | 43 | 9.9 | 860 | 3 | US-08-998-416-287 | Sequence 287, App |
| C 42 | 43 | 9.9 | 1141 | 3 | US-09-806-708B-22 | Sequence 22, App1 |
| C 43 | 43 | 9.9 | 16062 | 3 | US-09-949-016-13181 | Sequence 13181, A |
| C 44 | 42.8 | 9.8 | 601 | 3 | US-09-949-016-81304 | Sequence 81304, A |
| C 45 | 42.8 | 9.8 | 27757 | 3 | US-09-949-016-12407 | Sequence 12407, A |

ALIGNMENTS

RESULT 1
US-09-662-254B-23/C
Sequence 23, Application US/09662254B

GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Li, Yi
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
FILE REFERENCE: UF-221C1X1
CURRENT APPLICATION NUMBER: US/09/662,254B
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/086,651
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 50000
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
US-09-662-254B-23

Query Match 11.9%; Score 51.8; DB 3; Length 50000;
Best Local Similarity 51.3%; Pred. No. 0.018;
Matches 172; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

104 ATATCTAGTAAATTAATTAATGATGATCATGCAAGCAATTAATTAATCAGTTATTA 163
16973 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 16914
164 AACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 219
16913 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 16854
220 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 279
16853 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 16794
280 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 339
16793 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 16736
340 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 399

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 356.027 Seconds
(Without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-1

Perfect score: 435
Sequence: 1 gratacaatgactgcctaa.....aaatctgagtaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapect 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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3: geneseq1990s:*
4: geneseq2000s:*
5: geneseq2001as:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003cs:*
10: geneseq2003ds:*
11: geneseq2004as:*
12: geneseq2004bs:*
13: geneseq2004cs:*
14: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|-------|--------------------|-------------------|--------------------|
| 1 | 435 | 100.0 | 435 13 ADT08242 | Adt08242 Zebrafish |
| 2 | 435 | 100.0 | 435 13 ADT89050 | Adt89050 Zebrafish |
| 3 | 435 | 100.0 | 480 13 ADT08271 | Adt08271 Zebrafish |
| 4 | 435 | 100.0 | 480 13 ADT89079 | Adt89079 Zebrafish |
| 5 | 435 | 100.0 | 2033 13 ADT08244 | Adt08244 Zebrafish |
| 6 | 435 | 100.0 | 2033 13 ADT89052 | Adt89052 Zebrafish |
| 7 | 435 | 100.0 | 2783 13 ADT08243 | Adt08243 Zebrafish |
| 8 | 435 | 100.0 | 2783 13 ADT89051 | Adt89051 Zebrafish |
| 9 | 435 | 100.0 | 2960 13 ADT89080 | Adt89080 Zebrafish |
| 10 | 176.2 | 40.5 | 78064 13 ADT17402 | Adt17402 Nucleoid |
| 11 | 167.8 | 38.6 | 3003 10 ADP18692 | Adp18692 Zebrafish |
| 12 | 163.6 | 37.6 | 13382 14 ADW44488 | Adw44488 Zebrafish |
| 13 | 149.2 | 34.3 | 5563 2 AAX08941 | Aax08941 GATA-1 pr |
| 14 | 147.6 | 33.9 | 78064 13 ADT17402 | Adt17402 Nucleoid |
| 15 | 144 | 33.1 | 7495 13 ADP30815 | Adp30815 Zebrafish |
| 16 | 144 | 33.1 | 7508 13 ADK30814 | Adk30814 Zebrafish |
| 17 | 124.4 | 28.6 | 13382 14 ADW44488 | Adw44488 Zebrafish |
| 18 | 86.6 | 19.9 | 71843 8 ACC79619 | Acc79619 Zebrafish |
| 19 | 64.6 | 14.9 | 435 13 ADT08242 | Adt08242 Zebrafish |

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|------|------|------|----------|------------|---------------------|
| C 20 | 64.6 | 14.9 | 435 13 | ADT89050 | Adt89050 Zebrafish |
| C 21 | 64.6 | 14.9 | 480 13 | ADT08271 | Adt08271 Zebrafish |
| C 22 | 64.6 | 14.9 | 480 13 | ADT89079 | Adt89079 Zebrafish |
| C 23 | 64.6 | 14.9 | 2033 13 | ADT08244 | Adt08244 Zebrafish |
| C 24 | 64.6 | 14.9 | 2033 13 | ADT89052 | Adt89052 Zebrafish |
| C 25 | 64.6 | 14.9 | 2783 13 | ADT08243 | Adt08243 Zebrafish |
| C 26 | 64.6 | 14.9 | 2783 13 | ADT89051 | Adt89051 Zebrafish |
| C 27 | 64.6 | 14.9 | 2960 13 | ADT89080 | Adt89080 Zebrafish |
| C 28 | 62 | 14.3 | 98800 12 | ADN06353_3 | Continuation (4 of |
| C 29 | 62 | 14.3 | 98800 12 | ADN94372_3 | Continuation (4 of |
| C 30 | 55.8 | 12.8 | 517 13 | ACN56273 | ACN56273 Cotton an |
| C 31 | 55.4 | 12.7 | 9547 6 | ABL33504 | Ab132545 Human imm |
| C 32 | 55.2 | 12.7 | 7346 6 | ABL32345 | Ab132345 Human imm |
| C 33 | 52.4 | 12.0 | 16439 6 | ABL32887 | Ab155643 Ambp gen |
| C 34 | 51.8 | 11.9 | 50000 6 | ABL55643 | Abk28332 DNA trans |
| C 35 | 51.4 | 11.8 | 11745 6 | ABK28332 | Abk39955 Human che |
| C 36 | 51 | 11.7 | 8076 6 | ABK39955 | Abk39957 Human che |
| C 37 | 51 | 11.7 | 8136 6 | ABK39957 | Ab132555 Human imm |
| C 38 | 51 | 11.7 | 8136 6 | ABK32555 | Ab132555 Human imm |
| C 39 | 51 | 11.7 | 17897 10 | ADB54178 | Adb54178 Pretreat |
| C 40 | 51 | 11.7 | 17897 10 | ADB54178 | Adb89328 Oligonuc |
| C 41 | 50.8 | 11.7 | 14095 6 | ABL32477 | Ab132477 Human imm |
| C 42 | 50.6 | 11.6 | 6059 6 | ABL33460 | Ab133460 Human imm |
| C 43 | 50.6 | 11.6 | 15416 6 | ABL34231 | Ab1334231 Human imm |
| C 44 | 50.6 | 11.6 | 15416 6 | ABK31527 | Abk31527 Signal tr |
| C 45 | 50.6 | 11.6 | 15416 6 | ABL70498 | Ab170498 Chemical |

ALIGNMENTS

RESULT 1
ADT08242
ID ADT08242 standard; DNA; 435 BP.

AC ADT08242;

DT 13-JAN-2005 (first entry)

XX Zebrafish L-FABP upstream region -1983 to -1504.

XX Zebrafish; de; liver fatty acid binding protein; L-FABP;

KW liver regulatory element; LR; transgenic; HNF(1); HNF(2); HNF-1alpha;

KM HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;

KM liver development; liver disease; liver necrosis; liver cancer.

XX OS Danio rerio.

XX Key Location/Qualifiers

FT protein_bind 48..68

FT /*tag= a

FT /bound_molecly= "PDX1"

FT /*tag= b

FT /bound_molecly= "PDX1"

FT /*tag= c

FT /bound_molecly= "HNF-1alpha"

FT /*tag= d

FT /bound_molecly= "HNF-3beta"

XX US2004209833-A1.

XX 21-OCT-2004.

XX 21-NOV-2003; 2003US-00717573.

XX 16-APR-2003; 2003US-0463035P.

XX 27-MAY-2003; 2003US-0473210P.

XX (WUJ/J) WU J.

PA (HERG/) HER G M.

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 2587.9 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-7117-573-1

Sequence: 1 gtatacaatgacttgcctaa.....aaaatgtagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Maximum DB seq length: 20000000000

| | | |
|------------------|---------------|-----|
| Post-processing: | Minimum Match | 0% |
| | Maximum Match | 10% |

Listing first 45 summaries

Database :

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1:  gb_ba:*
2:  gb_in:*
3:  gb_env:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pr:*
9:  gb_ro:*
10: gb_sen:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hg:*
15: gb_pl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB | ID | Description |
|------------|-------|-------|--------------|----|-----------|-------------|
| 1 | 435 | 100.0 | 2960 | 5 | AF512998 | Danio rerio |
| 2 | 420.6 | 96.7 | 178271 | 5 | CR2993507 | Zebrafish |
| 3 | 223.2 | 51.3 | 85762 | 5 | CR3893368 | Zebrafish |
| 4 | 218 | 50.1 | 80017 | 5 | AL8453772 | Zebrafish |
| 5 | 218 | 50.1 | 150673 | 14 | CR361557 | Danio rerio |
| 6 | 208.8 | 48.0 | 137636 | 14 | CR788231 | Danio rerio |
| 7 | 206.8 | 47.5 | 153267 | 14 | CR354434 | Danio rerio |
| 8 | 206.2 | 47.4 | 191769 | 14 | CR933561 | Danio rerio |
| 9 | 205.8 | 47.3 | 169046 | 5 | AL928828 | Zebrafish |
| 10 | 204 | 46.9 | 162436 | 5 | AL928535 | Zebrafish |
| 11 | 203.8 | 46.9 | 171208 | 5 | BX296552 | Zebrafish |
| 12 | 203 | 46.7 | 231303 | 5 | BX649405 | Zebrafish |
| 13 | 202.2 | 46.5 | 165384 | 14 | CR391914 | Danio rerio |
| 14 | 202.2 | 46.5 | 203371 | 14 | AC139662 | Danio rerio |
| 15 | 202 | 46.4 | 154824 | 5 | BX323864 | Zebrafish |
| 16 | 202 | 46.4 | 153815 | 5 | CR392361 | Zebrafish |
| 17 | 202 | 46.4 | 192644 | 14 | CR762381 | Danio rerio |
| 18 | 202 | 46.4 | 221617 | 5 | BX530018 | Zebrafish |

| | | | | | | | |
|---|----|-------|------|---------|----|----------|--------------------|
| C | 19 | 201.6 | 46.3 | 156150 | 5 | BX322540 | BX322540 Zebrafish |
| C | 20 | 201.2 | 46.3 | 162129 | 5 | CR385025 | CR385025 Zebrafish |
| C | 21 | 201.2 | 46.3 | 1228771 | 14 | CR855129 | CR855129 Danio rer |
| C | 22 | 201.2 | 46.3 | 256437 | 5 | BX664629 | BX664629 Zebrafish |
| C | 23 | 201.2 | 46.3 | 304914 | 14 | BX342830 | BX342830 Danio rer |
| C | 24 | 200.8 | 46.2 | 222975 | 14 | CR848050 | CR848050 Danio rer |
| C | 25 | 199.8 | 45.9 | 190968 | 5 | BX465217 | BX465217 Zebrafish |
| C | 26 | 199.4 | 45.8 | 192117 | 5 | BX663603 | BX663603 Zebrafish |
| C | 27 | 199.2 | 45.8 | 226817 | 14 | CR855117 | CR855117 Danio rer |
| C | 28 | 199.2 | 45.8 | 222979 | 14 | CR931761 | CR931761 Danio rer |
| C | 29 | 199 | 45.7 | 113747 | 5 | BX004882 | BX004882 Zebrafish |
| C | 30 | 198.8 | 45.7 | 114105 | 14 | CR354589 | CR354589 Danio rer |
| C | 31 | 198.6 | 45.7 | 160087 | 5 | BX004867 | BX004867 Zebrafish |
| C | 32 | 198.4 | 45.6 | 173914 | 5 | BX279525 | BX279525 Zebrafish |
| C | 33 | 198.2 | 45.6 | 171719 | 5 | CR384061 | CR384061 Zebrafish |
| C | 34 | 198.2 | 45.6 | 150490 | 14 | CR450768 | CR450768 Danio rer |
| C | 35 | 198 | 45.5 | 215891 | 5 | AL928692 | AL928692 Zebrafish |
| C | 36 | 197.8 | 45.5 | 98234 | 5 | BX001026 | BX001026 Zebrafish |
| C | 37 | 197.4 | 45.4 | 149630 | 14 | CR628386 | CR628386 Danio rer |
| C | 38 | 197.4 | 45.4 | 164631 | 14 | BX901932 | BX901932 Danio rer |
| C | 39 | 197.4 | 45.4 | 165139 | 14 | CR925756 | CR925756 Danio rer |
| C | 40 | 197.4 | 45.4 | 184799 | 14 | CR936517 | CR936517 Danio rer |
| C | 41 | 197.4 | 45.4 | 186258 | 5 | BX640480 | BX640480 Zebrafish |
| C | 42 | 197.4 | 45.4 | 224691 | 14 | CR318603 | CR318603 Danio rer |
| C | 43 | 197.2 | 45.3 | 169758 | 5 | CR936240 | CR936240 Zebrafish |
| C | 44 | 197.2 | 45.3 | 174623 | 5 | BX005044 | BX005044 Zebrafish |
| C | 45 | 197 | 45.3 | 188775 | 14 | CR855313 | CR855313 Danio rer |

ALIGNMENTS

| | |
|------------|--|
| RESULT | 1 |
| AF512998 | 2960 bp DNA linear VRT 10-JUN-2003 |
| LOCUS | AF512998 |
| DEFINITION | Danio rerio liver-type fatty acid binding protein gene, partial cds. |
| ACCESSION | AF512998 |
| VERSION | AF512998.1 GI:21314558 |
| KEYWORDS | . |
| SOURCE | Danio rerio (zebrafish) |
| ORGANISM | Danio rerio Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 2960) Her.G.M., Yeh,Y.H. and Wu,J.L. 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish Dev. Dyn. 227 (3), 347-356 (2003) 12815620 2 (bases 1 to 2960) Her,G.M. and Wu,J.-L. Direct Submission Submitted (11-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan Location/Qualifiers 1..2960 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" <2784..>2960 /product="liver-type fatty acid binding protein" 2784..>2960 /note="tfabp; small cytosolic protein involved in lipid transport and metabolism" /codon_start=1 /product="liver-type fatty acid binding protein" /protein_id="AA047005.1" /db_xref="GI:21314559" /translation="WAFSGTWVAQENYEELRALSHPEEVKLVADVKEPTIEQN GSDPIITSKIRGTGYV" |
| CDS | |
| RNA | |
| FEATURES | |
| source | |
| JOURNAL | |
| PUBMED | |
| REFERENCE | |
| AUTHORS | |
| TITLE | |
| JOURNAL | |